Global and regional development of the human cerebral cortex

Global and regional development of the human cerebral cortex: molecular architecture and occupational aptitudes

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Running title: Global and regional development of the human cerebral cortex

Abstract

We have carried out meta-analyses of genome-wide association studies (n=23,784) of the first two principal components (PCs) that group together cortical regions with shared variance in their surface area. PC1 (global) captured variations of most regions, whereas PC2 (visual) was specific to the primary and secondary visual cortices. We identified a total of 18 (PC1) and 17 (PC2) independent loci, which were replicated in another 25,746 individuals. The loci of the global PC1 included those associated previously with intracranial volume and/or general cognitive function, such as *MAPT* and *IGF2BP1*. The loci of the visual PC2 included *DAAM1*, a key player in the planar-cell-polarity pathway. We then tested associations with occupational aptitudes and, as predicted, found that the global PC1 was associated with General Learning Ability, and the visual PC2 was associated with the Form Perception aptitude. These results suggest that inter-individual variations in global and regional development of the human cerebral cortex (and its molecular architecture) cascade – albeit in a very limited manner – to behaviours as complex as the choice of one's occupation.

Keywords: brain development, cortical surface area, cortical thickness, genome-wide association study, occupational aptitude

Introduction

The radial unit hypothesis provides a framework for global and regional expansion of the primate cerebral cortex (Rakic 1988). Using magnetic resonance imaging (MRI), one can derive a number of metrics informative with regard to development and aging of the human cerebral cortex, including cortical surface area and cortical thickness. The two measures provide insights into different developmental processes, each with a different timeline. Cortical surface area reflects primarily the tangential growth of the cerebral cortex during prenatal development; the phase of *symmetric division of progenitor cells* in the proliferative zones during the first trimester is particularly important for the tangential growth through additions of ontogenetic columns (Rakic 1988). The subsequent phase of *asymmetric division* continues to increase the number of ontogenetic columns (and thus surface area) but it also begins to contribute to the thickness of cerebral cortex formed by post-mitotic neurons migrating from the proliferative zones to the cortical plate in the inside-out manner (Rakic 1988). Ionizing radiation of the (monkey) fetus during early gestation reduces surface area (sparing cortical thickness) while the same radiation applied in mid-gestation affects both the surface area and cortical thickness (Selemon et al. 2013). While surface area remains stable after early childhood, cortical thickness continues to change, in particular during puberty and aging. Furthermore, both surface area and cortical thickness vary across individuals in global and regional manners.

In recent years, substantial progress has been made in revealing molecular architecture of a number of brain phenotypes, including those captured by global (e.g., intracranial volume (Adams et al. 2016)) and regional (e.g., hippocampal volume(Stein et al. 2012)) measures derived from T1-weighted MR images, as well as other MRI-derived brain phenotypes (e.g., inter-hemispheric connectivity (Mollink et al. 2019)). Recent efforts of the CHARGE (Hofer 2018) and ENIGMA (Grasby 2018) Consortia have focused on identifying genetic variations associated with values of surface area and thickness at each of the 34 cortical regions delineated by FreeSurfer. Given the previously observed genetic influences on both surface area (Chen et al. 2012) and thickness (Chen et al. 2013) across multiple regions of the human cerebral cortex, we took a different approach and performed, first, principal component analysis of the surface area and thickness of the 34 cortical regions and, then, executed genome-wide association studies (GWAS) of these derived cortical phenotypes, namely the first two principal components of surface area and thickness, respectively. We meta-analyzed these in a total of 23,784 individuals (with replications in another 25,746 individuals). Finally, as a proof of concept, we asked whether inter-individual differences in the derived cortical phenotypes relate to behaviours as complex as the choice of one's occupation. To achieve this, we took advantage of a unique resource, the Dictionary of Occupational Titles (National Research Council 1980), and related both the brain phenotypes and their genetic determinants to relevant occupational aptitudes in up to 220,000 individuals.

Materials and Methods

Participants

For the meta analyses of GWASs of principal components of cortical surface area and thickness across the 34 regions of interest, we analyzed data of the 23,784 participants from 19 cohort studies collaborating in the Cohorts of Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium (Psaty et al. 2009) and the UK Biobank (UKBB) (Sudlow et al. 2015). All the individuals, aged between 12 and 97 years, were stroke- and dementia-free and of European ancestry. Table E1 provides the information on demographic characteristics, brain imaging measures and acquisition, and

genotyping for each cohort study. Each study secured approval from institutional boards or equivalent organizations, and all participants provided written informed consent. Our meta-GWAS results were replicated in participants from ENIGMA consortium and an independent subset of UKBB participants who were not included in our meta-GWAS analyses (total N = 25,746). For the association analyses of occupational aptitudes vs. brain phenotypes and genetic variants, we analyzed up to 220,000 UKBB participants.

Principal Component Analysis of Cortical Surface Area and Cortical Thickness

Each cohort estimated the surface area (left and right hemispheres summed) and the thickness (left and right hemispheres averaged) of the 34 cortical regions, using FreeSurfer (Fischl and Dale 2000) or FSL FIRST (Patenaude et al. 2011) and carried out principal component analyses to obtain the loadings of the first two leading components PC1 and PC2 (see Figures E1 and E2 for cohort-specific loadings for the surface area and thickness, respectively). Then, for each cortical region, median value of loadings was obtained across the cohorts. The median loading values (Table E2) were then used to derive the 'general' PC score for each individual (script available at https://doi.org/10.6084/m9.figshare.11619879) and later used as the outcome variable in the multiple linear regression models fitted for the GWAS analyses.

Genome-wide Association Studies and Meta-Analyses

The GWAS and meta-analyses were carried out as follows. Using the median PC loadings across the CHARGE consortium cohorts (Figures E1 and E2; Table E2), each cohort derived the 'general' PC1 and PC2 scores for the Surface Area and the Thickness (PC1-SA, PC2-SA, PC1-TH and PC2-TH) to be used as phenotypes in the genome-wide association tests in order to ensure 'homogeneity' in phenotype derivation. All the association tests were adjusted for age, sex and other cohort-specific confounding variables, such as study site and/or family structure. The cohort-specific GWAS results were then examined for quality control with Easy QC software (Winkler et al. 2014), and meta-analyzed with METAL (Willer et al. 2010) using fixed effects models. Quantile-quantile plots of associations yielded by the genome-wide association study meta-analyses are shown in Figure E3. Results were inspected for inflation due to confounders such as population stratification or sample overlap, by calculating the inflation factor (λ) as well as the LD score intercept using LD score regression (Bulik-Sullivan et al. 2015b). An inflation factor $\lambda > 1$ suggests an inflation of the association statistics, which can be due to both spurious and genuine effects. It is likely to increase with sample size and degree of polygenicity of the phenotype, as the distribution of effect sizes begins to differ substantially from a null distribution when more variants have true associations. An LD score intercept > 1 suggests that there is spurious association, but an intercept <1.10 is generally considered to suggest that the signal is mostly due to genuine association effects. LD score regression intercepts were 1.05 (se=0.0079), 1.03 (se=0.0076), 1.03 (se=0.0065) and 1.02 (se= 0.007), for PC1-SA, PC2-SA, PC1-TH and PC2-TH, respectively.

Replication analyses were carried out in an independent subset of 6,234 UKBB participants, who were not included in the meta-GWAS, and '*in-silico*' based on the ENIGMA3-GWAS summary statistics for the surface area of the 34 FreeSurfer-cortical regions of interest in 19,152 participants of European ancestry from 34 cohorts (Grasby 2018). The *in-silico*' replication analysis was done using the genome-wide inferred statistics (GWIS) approach (Nieuwboer et al. 2016). In particular, the ENIGMA3 meta-GWAS summary statistics and the median PC loadings used to derive the PC-scores in our meta GWAS were used to derive the coefficient estimates and their corresponding

standard errors, using delta-method. We then performed a look-up of the SNPs associated with PC1- and PC2-SA in those summary GWIS-statistics.

Gene Expression in the Human Cerebral Cortex

We examined temporal and spatial pattern of gene expression using the BrainSpan atlas (www.brainspan.org). The mRNA expression levels were measured by RNA sequencing in 607 brain tissues from 18 female and 23 male donors. Table E4 in Extended Data provides details about the donor brains and the sample brain regions. Authors of the original report describing these data surveyed 10 potential confounders of the variation in gene expression using the top 10 components yielded by a multidimensional scaling analysis, namely age, brain region, sequence depth, pH, RNA integrity number (RIN), sex, ethnicity, hemisphere, sample dissection score and sequencing processing site; as reported in Fig. S11B of the original report, “only age and brain region correlated strongly with specific dimensions” (Li et al. 2018).

Genetic Correlations

Genetic correlations were conducted between PC1-SA and PC2-SA (surface area PC scores) and complex traits (growth, brain function and brain disorders) using LD score regression method for genetic correlation estimation using summary GWAS summary statistics and LD structure (Bulik-Sullivan et al. 2015a) implemented in LDSC v1.0.0 (https://github.com/bulik/ldsc). Single nucleotide polymorphisms (SNPs) were filtered using the available HapMap3 SNPs and genetic correlations were conducted using LDSC's 1000 Genomes European LD scores. Genetic correlations were restricted to European GWAS samples (Table E10). A Bonferroni correction was applied to correct for the 55 genetic correlations. The required LDSC files were obtained from the LDSC GitHub repository (https://data.broadinstitute.org/alkesgroup/LDSCORE/).

Partitioned Heritability

This analysis was conducted using LD score regression method for partitioaned heritability estimation (Finucane et al. 2015) implemented in LDSC v1.0.0 (https://github.com/bulik/ldsc) in order to assess the enrichment of PC1-SA and PC2-SA GWAS variants in chromatin regions with differential accessibility during cortical neurogenesis between the germinal zone (GZ) and cortical plate (CP), as reported previously for other phenotypes(de la Torre-Ubieta et al. 2018). Enrichment of heritability represents the ratio between (i) the proportion of heritability explained by a particular annotation and (ii) the proportion of SNPs in the annotation (de la Torre-Ubieta et al. 2018; Finucane et al. 2015). An annotation file was generated for regions in which chromatin was more accessible in GZ, compared to CP (GZ>CP; 19,260) and vice-versa (CP>GZ; 17,803), using the available supplementary data table (de la Torre-Ubieta et al. 2018). Next, LD scores for the chromatin annotation file were computed following the LDSC guidelines (https://github.com/bulik/ldsc/wiki/LD-Score-Estimation-Tutorial), using the available HapMap3 SNPs, a 1 cM window, and the Phase 3 1000 Genomes European genotype files. Finally, partitioned heritability was run combining the chromatin annotation file with the LDSC baseline annotation file. The required LDSC files were obtained from the LDSC GitHub repository (https://data.broadinstitute.org/alkesgroup/LDSCORE/).

Occupational Aptitudes

We used the Dictionary of Occupational Titles [DOT] (National Research Council 1980) that contains 28,801 titles of which 12,099 are so-called “base” titles (corresponding to occupations). Each base title is associated with scores capturing, among other things, aptitudes defined as “the capacities or abilities required of a worker to facilitate the

learning of job tasks" (p. 29 (National Research Council 1980)); DOT contains scores for a total of 11 aptitudes, including General Learning Ability and Form Perception. In DOT, General Learning Ability was defined as "The ability to "catch on" or understand instructions and underlying principles; the ability to reason and make judgments. Closely related to doing well in school" (p. 9-3 (National Research Council 1980)). Form Perception aptitude was defined as "The ability to perceive pertinent details in objects or in pictorial or graphic material. Ability to make visual comparisons and discrimination and see slight differences in shapes and shadings of figures and widths and lengths of lines" (p. 9-17 (National Research Council 1980)). To test these predictions, we used the data on occupations of the UK Biobank participants with available MRI data (n=21,609). The UK BioBank encodes occupation using the UK 2000 Standard Occupation Classification [SOC2000UK] (Office for National Statistics 2000), while aptitude scores are associated with DOT (National Research Council 1980). A crosswalk, or mapping, from the SOC2000UK codes to the DOT codes was required in order to assign occupational aptitude scores to each participant. As a direct mapping was not available, we combined several available mappings: SOC2000UK to the 2010 version [SOC2010UK] (Office for National Statistics 2010b; 2012), SOC2010UK to the 2008 International Standard Classification of Occupations [ISCO2008] (International Labour Office 2012; Office for National Statistics 2010a), ISCO2008 to the US 2010 Standard Occupational Classification [SOC2010US] (Cosca and Emmel 2010; Emmel and Cosca 2010; Labor and Statistics), and SOC2010US to DOT (http://www.widcenter.org/document/legacy-crosswalks/). For a given SOC2000UK code, all of the matching SOC2010UK codes were found, and for each of these, all of the matching ISCO2008 codes were found; this procedure was repeated for each subsequent crosswalk. Thus, each SOC2000UK code could be associated with many DOT codes. The aptitude scores associated with each SOC2000UK code were the average of the aptitude scores associated with each corresponding DOT code (DOT codes without an associated aptitude were ignored).

Associations with Polygenic Scores for Surface Area PC1 and PC2

Polygenic scores for surface area PC1 and PC2 in the UK Biobank participants were calculated based on the GWAS significant SNPs (with $p < 5E-08$) identified from our meta-GWAS analyses, using PRSice (Euesden et al. 2015). In the UK Biobank genotype data, we identified the 78 (for PC1-SA) and 55 (for PC2-SA) SNPs. After clumping based on LD ($r^2 < 0.1$), the final scores were obtained using the 16 and the 14 independent SNPs, respectively, for PC1-SA and PC2-SA. Associations for the polygenic scores for PC1-SA were tested with the respective PC scores, and with the General Learning Ability and the Form Perception aptitude, using multiple linear regression models. For the regression models, the outcome variable was either PC-SA score or ability/aptitude value, and the predictor variable was the polygenic score, both of which were standardized (i.e., z-scored) so that the coefficient for the polygenic score can be interpreted as the number of standard deviations the outcome increases for every standard deviation increase in the polygenic score, holding all the other covariates constant. All the analyses were adjusted for age, sex and/or MRI site. The association tests for the Form Perception aptitude variable were additionally adjusted for General Learning Ability.

Results

Participants

Here we report findings obtained in 23,784 participants assessed across 19 cohorts from the CHARGE Consortium and the UK Biobank (Table E1 in Extended Data), and replicated in a subsequent release of the UK Biobank participants (n=6,234) as well as

in silico(Nieuwboer et al. 2016) using region-based summary statistics provided by the ENIGMA Consortium (n=19,512).

Principal Component Analysis of Cortical Phenotypes

To identify components of shared variance of the surface area and of the thickness of the cerebral cortex, we have carried out principal component analyses of regional values of surface area and of thickness (34 regions segmented by FreeSurfer or FSL FIRST [in 2 cohorts]) in each cohort. For surface area and thickness, respectively, the first (PC1) and second (PC2) components were loaded by similar sets of cortical regions across all 13 cohorts available for loading calculations (Figures E1 [surface area], E2 [cortical thickness] and Table E2 in Extended Data). Figure 1 illustrates the median loadings for each of the 34 cortical regions in PC1 (Figure 1A) and PC2 (Figure 1B) for surface area. Note that PC2 includes only a handful of cortical regions in the medial aspect of the occipital lobe, including the pericalcarine (primary visual) cortex.

Genome-wide Association Studies and their Meta-analysis

We then executed a GWAS in each of the 19 cohorts and, subsequently, meta-analyzed these cohort-based results for each of the four phenotypes, namely PC1 and PC2 of surface area, and PC1 and PC2 of thickness.

For surface area, the first (global) component was associated with 42 independent SNPs in 18 independent loci (Table E3, in Extended Data). The strongest signal was found in a broad region of chromosome 17, which contained a number of genes, including those associated previously with intracranial volume (Adams et al. 2016; Hibar et al. 2015) and/or general cognitive function(Trampush et al. 2017) (Figure 2, Table E4A in Extended Data). The second (visual) component was associated with 57 SNPs in 17 independent loci (Table E3, in Extended Data). The strongest signal was found at a locus on chromosome 14 containing *DAAM1* (Figure 3, Table E4B in Extended Data). We replicated 695/807 (global PC1) and 952/1,155 (visual PC2) GWAS-significant SNPs (Tables E4A and E4B, in Extended Data).

For cortical thickness, meta-GWAS identified no locus associated with PC1 and one independent SNP in 1 locus on chromosome 15 associated with PC2 (Figure E4).

Genomic landscape and genome biology of the main genetic loci

Next, we focus on the two genetic loci containing SNPs with the strongest associations with the cortex-wide (global PC1) and regional (visual PC2) variations in the cortical surface area on chromosomes 17 and 14, respectively (Figures 2 and 3).

The locus on chromosome 17, associated with the global component of surface area (PC1), spans 4.5 Mb and contains 10 protein-coding genes (Figure 2A). Given that surface area is determined mainly by the growth of the human cerebral cortex (most pronounced before birth), we have examined spatio-temporal pattern of their expression using the BrainSpan dataset (Table E5 in Extended Data). As shown in Figure 4A, only 2 of the 10 protein-coding genes within this locus show high levels of expression in the entire cerebral cortex during the prenatal period: *IGF2BP1* (Insulin Like Growth Factor 2 MRNA Binding Protein 1) and *MAPT* (Microtubule Associated Protein Tau). Other genes either show low expression during this period (e.g., *ARHGAP27*) or appear to be expressed only in subcortical structures (e.g., *WNT3*). Next, we have examined several publically available databases to ascertain whether top SNPs in/near the two genes could influence their expression. *IGF2BP1* "functions by binding to the mRNAs of certain genes, including insulin-like growth factor 2, beta-actin and beta-transducin repeat-containing protein, and regulating their translation" (Stelzer et al. 2016). The top SNP

(rs11079849) lies in an enhancer/promoter region of *IGF2BP1* in fetal brain and alters regulatory motifs of several transcription factors (Ward and Kellis 2012). The most differential binding affinity occurs for specificity protein 2 transcription factor (SP2), a cell cycle regulator in neural stem and progenitor cells (Liang et al. 2013). This top SNP is also associated with differential methylation at 16 CpGs located within 1Mbps of the SNP (chr17: 46,908,359-47,102,000) (Gaunt et al. 2016). The minor allele (T, associated with higher values of PC1) is associated with lower DNA methylation in the promotor region of *IGF2BP1*. *MAPT* "Promotes microtubule assembly and stability, and might be involved in the establishment and maintenance of neuronal polarity" (Stelzer et al. 2016). The top SNP (rs62056789) is found in the promotor/enhancer regions in fetal brain (Ward and Kellis 2012) and, via motif change, is in a position to influence binding affinity of Forkhead box (Fox) transcription factors, such as FOXF1 and FOXF2, that play important roles in regulating expression of genes involved in cell growth, proliferation, differentiation and longevity (Tuteja and Kaestner 2007a; 2007b). In addition to FOX-family transcription factors, the top SNP's LD-proxy (rs625056790, r^2=1) alters motifs for POU3F2, a POU-homeodomain transcription factor shown to have a critical role in neuronal differentiation in mouse brain (Nakai et al. 1995). The top SNP is also associated with differential methylation at 35 CpG sites located within 1Mbp of the SNP (chr17: 43,099,144-44,439,469) (Gaunt et al. 2016). The minor allele (C, associated with lower values of PC1) is associated with lower DNA methylation of CpGs in the promotor region and higher methylation of CpGs in the enhancer regions of *MAPT*. Finally, we evaluated the spatio-temporal pattern of co-expression of the two genes in the cerebral cortex during the prenatal period, followed by the assessment of gene enrichment using Gene Ontology. Using the BrainSpan dataset (Table E5 in Extended Data; prenatal period, cerebral cortex), we carried out a co-expression analysis for each of the two genes, and retained the top 1% genes whose expression varied in time (8 to 37 post-conception weeks) and space (11 cortical regions) in the same directions as the seed gene (*IGF2BP1 or MAPT)* for gene-ontology analysis using the PANTHER overrepresentation test tool (Mi et al. 2019). The *IGF2BP1* co-expression network (555 genes) is enriched for a number of biological processes related to cell division (e.g., mitotic G2/M transition checkpoint, DNA replication, negative regulation of DNA endoreduplication), gene transcription (e.g., regulation of transcription by RNA polymerase II) and translation (regulation of gene silencing by miRNA); see Table E6 in Extended Data. The *MAPT* co-expression network (424 genes) is enriched for a number of biological processes related to neurite development (e.g., regulation of neuron projection development, regulation of axon extension, axon development), axonal transport (e.g., axonal transport, organelle transport along microtubule) and neurotransmission (synaptic vesicle exocytosis, glutamate secretion); see Table E7 in Extended Data.

The locus on chromosome 14, associated with the regional – visual cortex – component of surface area (PC2) contains a single gene, namely *DAAM1* (Figure 3). This gene is a key component of the planar-cell-polarity signaling pathway (Beane et al. 2012; Tissir and Goffinet 2010); it acts as a bridging factor between Disheveled, Rho-family GTPases and Rho-associated kinases (Habas et al. 2001), a molecular complex involved in organizing actin cytoskeleton (Yang and Mlodzik 2015). As shown in Figure 4B, *DAAM1* is expressed in the human cerebral cortex between ~80 and ~150 post-conception days; after birth, its expression is very low. Note that, in monkeys, neurogenesis of the primary visual cortex begins around embryonic day 40 (E40) and ends at E100 (165-day gestation) (Rakic 1988). There are multiple lines of evidence supporting the notion that the dates of neurogenesis in macaque can be translated to

those in human (Zhu et al. 2018). Based on models for matching neurodevelopment across species, a neurogenesis event in the cerebral cortex of the Rhesus Macaque at post-conception day 50 translates to post-conception day 55 in the Human (http://translatingtime.org/translate (Workman et al. 2013).

Next, we have examined several publicly available databases to ascertain whether top SNPs in/near *DAAM1* could influence its expression. Based on HaploReg (Ward and Kellis 2012) analysis, the top SNP (rs73313052) is found in an enhancer region. According to the mQTL Database (Gaunt et al. 2016), the *DAAM1* top SNP did not have any differentially methylated CpGs within 1Mbp; but SNPs in strong linkage disequilibrium (LD) with the top SNP (r2 >0.6) are associated with differential methylation at two CpG sites, cg18819791 and cg22995959. The minor allele of the top SNP (A, associated with lower values of PC2) is associated (via its proxy) with higher DNA methylation at these two CpG sites, which may influence *DAAM1* expression; one can predict lower expression values in the carriers of the rs73313052_A minor allele. Finally, as above, we examined co-expression of *DAAM1* across all cortical regions and prenatal time points using the same BrainSpan dataset. As expression of *DAAM1* increases, so does expression of genes enriched in pathways involving neuron migration and cytoskeleton organization, among others (Table E8 in Extended Data). To ascertain the pattern of *DAAM1* co-expression *specific* to the primary visual cortex (V1), we have identified genes co-expressed highly (top 1%) in V1 but not in any other cortical region (i.e., not present among top 1% in any of the other eight regions). This analysis yielded striking enrichment for mitochondria-related genes co-expressed strongly in the same direction as *DAAM1* in V1 but not in the other cortical regions (Table E9 in Extended Data). This observation turned our attention to the well-known parcellation of the visual cortex to cytochrome-oxidase rich sub-regions, so-called “blobs” (V1) and “stripes” (V2/V3) (Livingstone and Hubel 1982). We then examined co-localization of *DAAM1* and a mitochondrial marker ATP5A in the developing (22nd post-conception week) visual cortex (Figure E5); its co-localization is consistent with the co-expression analyses described above.

Genetic Correlations with Relevant Complex Traits

We evaluated similarities in the genetic architecture of the global PC1 and the visual PC2 of surface area with that of several traits studied by GWAS in a large number of individuals (n>20,000). We focused on traits related to general growth (birth weight, adult height), brain function (global cognition, educational attainment), and several brain disorders (attention deficit hyperactivity disorder, schizophrenia, bipolar disorder, major depressive disorder, and late-onset Alzheimer’s disease; see Table E10 for the GWAS sources). As shown in Figure 5 (see also Table E11 in Extended Data), the SNPs associated with the global PC1 overlapped with SNPs associated with the general growth and brain function but not with any psychiatric disorders. This was not the case for the regional growth of the cerebral cortex (PC2); none of the assessed traits showed genetic correlations (after correction for multiple comparisons). This pattern is consistent with the enrichment of biological processes implicating cell proliferation (e.g., centrosome duplication, chromosome separation) and early brain development (e.g., neural tube closure, brain morphogenesis) in a gene set co-expressed (during prenatal development) with genes associated with PC1 (Table E12A; Extended Data); note, nonetheless, that a number of biological processes are equally enriched for the PC1- and PC2-based co-expression datasets (e.g., mitotic nuclear division, neurogenesis; Table E12B). Note also that SNP-based heritabilities for surface area PC1 and PC2 were enriched in genomic regions with higher accessibility in the germinal zone (vs.

cortical plate), as identified by de la Torre-Ubieta and colleagues (de la Torre-Ubieta et al. 2018) (Table E13).

Associations with Occupational Aptitudes

As a proof of concept, we have tested the possibility that the global and regional components, and/or their molecular architecture, predict complex behavior captured by the individual's occupation. We took advantage of the Dictionary of Occupational Titles [DOT] (National Research Council 1980) that contains 28,801 titles of which 12,099 are so-called "base" titles (corresponding to occupations). Each base title is associated with scores capturing, among other things, aptitudes defined as "the capacities or abilities required of a worker to facilitate the learning of job tasks" (p. 29 (National Research Council 1980)); DOT contains scores for a total of 11 aptitudes, including General Learning Ability and Form Perception, where lower values indicating greater ability/aptitude (range: 1 to 5). We chose to test the relationship between the global component (PC1) and the General Learning Ability based on the observed genetic correlation between PC1 and educational attainment (see above). We predicted that individuals with larger PC1 would be more likely to hold occupations associated with a greater General Learning Ability, defined as "The ability to "catch on" or understand instructions and underlying principles; the ability to reason and make judgments. This is closely related to doing well in school" (p. 9-3 (National Research Council 1980)). We chose to test the relationship between the regional (visual) component (PC2) and Form Perception based on comparative studies of the primate visual cortex. These studies suggest that a larger primary visual cortex (containing more neurons) can process visual information with a greater granularity(de Sousa and Proulx 2014). Thus, a model proposed by de Sousa and Proulx states that "the size of visual field represented by a neuron is inversely related to the size of the cortical region"(de Sousa and Proulx 2014). We predicted that individuals with a larger PC2 would be more likely to hold occupations associated with a greater Form Perception aptitude, defined as "The ability to perceive pertinent details in objects or in pictorial or graphic material. Ability to make visual comparisons and discrimination and see slight differences in shapes and shadings of figures and widths and lengths of lines" (p. 9-17 (National Research Council 1980)). Given that greater aptitude for Form Perception is found in occupations requiring also greater General Learning Ability, General Learning Ability can be either a precision or a confounding variable. Hence, in order to increase statistical power or prevent spurious inference, we adjusted for this variable, in addition to sex and age, when testing the association between Form Perception aptitude and PC2. To test these predictions, we used data on occupations of the UK Biobank participants with available MRI data (n=21,609), and linked the (UK) Standard Occupation Codes (Office for National Statistics 2000) with the DOT codes (National Research Council 1980). To increase homogeneity of this sample, we included only participants classified as "White" in the UK Biobank database (a combination of self-reported ethnicity and genetic principal components; n=18,890). Both MRI and occupation data were available in 12,829 of these individuals. In this sample, PC1 was associated with General Learning Ability (beta=-0.08; t=-8.4, *P*=3.6E-17; adjusted for sex and age). PC2 was associated with Form Perception aptitude (beta=-0.0059; t=-2.5, p=0.014; adjusted for sex, age and General Learning Ability, which correlates with Form Perception aptitude [r=0.38, p<0.001]). In both cases, higher values of the principal components (i.e., higher global and regional surface area) predicted higher values of the respective occupational aptitudes. We then tested associations between PC1-related *MAPT* (rs62056789) and PC2-related *DAAM1* (rs2164950, an LD-proxy of [the imputed] rs73313052, r^2=1) and, respectively, General Learning Ability and Form Perception aptitude in all UK Biobank

("white") individuals with both occupation and genetic data (n=222,562). For *MAPT* (rs62056789), we observed an association between General Learning Ability and this polymorphism (p = 8.3E-10, $\beta = -0.013$, t = -6.1; adjusted for sex and age). For *DAAM1* (rs2164950), we observed no association between Form Perception aptitude and this polymorphism (p = 0.24, $\beta = -0.0022$, t = -1.2; adjusted for sex, age and General Learning Ability).

Associations with Polygenic Scores for Surface Area PC1 and PC2

As a proof of concept, we derived polygenic scores based on the GWAS-significant SNPs identified from surface area PC1 and PC2 meta-GWAS, and tested their associations with the respective phenotypes in UK Biobank "White" participants (n=18,036). As expected, the polygenic scores were strongly correlated with the PC1 scores (p = 4.8E-55, β= 0.095, t = 15.7; adjusted for age, sex and MRI site) and PC2 scores (p = 8.5E-107, β= 0.16, t = 22.1; adjusted for age, sex, MRI site). Finally, in all "White" UK Biobank participants with both the genetic and occupational data (n=249,690), we tested for the relationship between polygenic scores and the two occupational aptitudes. The polygenic score for PC1 was strongly associated with General Learning Ability in the expected direction, namely higher polygenic score predicted higher ability (p = 8.4E-14, β= -0.015, t = -7.5; adjusted for age and sex). We observed no association between Form Perception and the polygenic score for PC2 (p = 0.77, β= -0.0005, t = -0.3; adjusted for age, sex and General Learning Ability).

Discussion

Here we discovered a non-overlapping set of 99 'independent' SNPs contributing to the global and regional tangential growth of the human cerebral cortex. On the other hand, our meta-GWAS of cortical thickness, carried out in the same individuals, yielded only one locus. This negative finding (similar to those reported by the CHARGE (Hofer 2018) and ENIGMA (Grasby 2018) Consortia) may reflect substantial dynamics of cortical thickness during puberty (Walhovd et al. 2017) and aging (Vinke et al. 2018), and the contribution of different genetic variants throughout the lifespan.

The robustness of our findings with regard to surface area is remarkable. It is likely that this phenotype – measured in adults of different ages – provides a high-fidelity proxy of prenatal and early post-natal brain development. As reviewed previously, surface area of the human cerebral cortex reaches its peak around 2 years of age (Gilmore et al. 2018); it remains relatively stable throughout adulthood (less than 4% decrease between 40 and 80 years of age in our UK Biobank sample). The developmental origin of this phenotype is reflected in the results of our meta-GWAS in several respects. First, many genes associated with variations in surface area are highly expressed during prenatal development; expression of *DAAM1* is a prime example in that its expression peaks during mid-gestation and decreases to negligible levels by birth. Second, genes co-expressed with the three genes studied here in more detail (i.e., *MAPT*, *IGF2BP1* and *DAAM1*) are enriched for biological processes associated with cell growth (e.g., regulation of cell cycle). Third, genetic variants associated with both the global PC1 and visual PC2 are enriched in chromatin regions with higher accessibility in the germinal zone (vs. cortical plate) in the fetal (human) brains.

The global (PC1) component yielded a set of consistent results. First, the main genetic locus (chromosome 17) associated with this component has been observed previously in our meta-GWAS of intracranial volume (Adams et al. 2016); intracranial volume correlates strongly with surface area. Second, genetic variations associated with this component overlap with a number of traits related to both the overall growth of the body,

namely birth weight and adult height, but also with traits associated with cognitive abilities, namely educational attainment and cognitive function. Third, using occupational aptitudes, we have confirmed the latter by showing a strong association between the global PC1 and General Learning Ability, a trait expected to relate strongly to educational attainment. It is also of note that General Learning Ability was associated with genetic variations in *MAPT*, one of the genes in the chromosome 17 locus. Mutations in this gene occur more frequently in patients with fronto-temporal dementia (Ciani et al. 2019; Strang et al. 2019).

The visual (PC2) component provided an unexpected set of new insights. To start with, the grouping of the primary and secondary visual cortices by their shared variance in surface area suggests that a set of common processes guiding their development may be, to a certain extent, distinct from those involved in the global cortical growth. Experimental work in non-human primates points strongly to the eye as a source of this distinction: removing the eyes during fetal development decreases the surface area of the visual cortex (Bourgeois and Rakic 1996; Dehay et al. 1996). This effects is consistent with a tight relationship between the volume of the lateral geniculate nucleus (LGN) and the surface area of the primary visual cortex in the human (adult) brain, as assessed post mortem (Andrews et al. 1997). In both cases, it is likely that waves of spontaneous activity in the retina (Feller et al. 1996; Shatz and Stryker 1988), transmitted to the developing cortex via LGN, play a key role in mediating these effects. At a molecular level, our meta-GWAS of the visual PC2 revealed a robust association in a genetic locus containing *DAAM1*. *DAAM1* is a key component in the planar-cell-polarity signaling pathway (Beane et al. 2012; Tissir and Goffinet 2010); it acts as a bridging factor between Disheveled, Rho-family GTPases and Rho-associated kinases (Habas et al. 2001), a molecular complex involved in organizing actin cytoskeleton (Yang and Mlodzik 2015). We showed that *DAAM1* is highly expressed between 12th and 22nd post-conception weeks in the human cerebral cortex, and that genes co-expressed with *DAAM1* in the primary visual cortex are enriched in mitochondria-related pathways. We formulated a working model by which *DAAM1* regulates tangential expansion of the visual cortex by interacting with LGN inputs, likely at the level of cortical subplate, during mid-gestation.

A larger visual cortex is likely to possess more inter-hemispheric connections; *DAAM1* polymorphism is associated with a structure-predicted functional connectivity of the human visual cortex (Mollink et al. 2019). Comparative studies in non-human primates also suggest that a larger primary visual cortex contains a larger number of neurons and, in turn, a more fine-grained representation of the visual field (de Sousa and Proulx 2014). It has been shown, in both human and non-human primates, that species/individuals with a larger visual cortex are less prone to size illusions (e.g., Ebbinghaus illusion), possibly due to less of an overlap between visual representations of the central object and the surrounding context (de Sousa and Proulx 2014; Schwarzkopf et al. 2011). Our findings of a significant – albeit weak – relationship between the visual PC2 and Form Perception aptitude are consistent with a more granular visual representation in individuals with a larger visual cortex.

Overall, these findings illustrate how specification of cortical areas, and their relative growth, might be guided by an interaction between fetal environment and generic developmental mechanisms, such as those constituting planar-cell-polarity signaling pathway. They also illustrate that inter-individual variations in global and regional development of the human cerebral cortex (and its molecular architecture) can cascade

– albeit in a very limited manner – to behaviours as complex as the choice of one's occupation.

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R. Weinberger (Lieber Institute for Brain Development, Baltimore, USA), Margaret J. Wright (Queensland Brain Institute, University of Queensland, St Lucia, Australia), Juan Zhou (Center for Cognitive Neuroscience, Neuroscience and behavioral disorders program, Duke-National University of Singapore Medical School, Singapore, Singapore), Jason L. Stein (Department of Genetics & UNC Neuroscience Center, University of North Carolina at Chapel HIll, Chapel Hill, USA), Paul M. Thompson (Imaging Genetics Center, Mark and Mary Stevens Neuroimaging and Informatics Institute, Keck School of Medicine of USC, University of Southern California, Los Angeles, USA), Sarah E. Medland (Psychiatric Genetics, QIMR Berghofer Medical Research Institute, Brisbane, Australia).

Figure legends

Figure 1. Lateral and medial views of median unrotated principal component (PC) loadings for the surface area of the 34 cortical regions in CHARGE consortium cohorts. Lateral (left column) and medial (right column) views of the median PC loadings are shown for PC1 (top) and PC2 (bottom). The red-to-blue color indicates the positive-to-negative loading values (i.e., correlation between PC scores and raw data) as indicated by the color bar. The regional median PC-loading values are shown in Table E2.

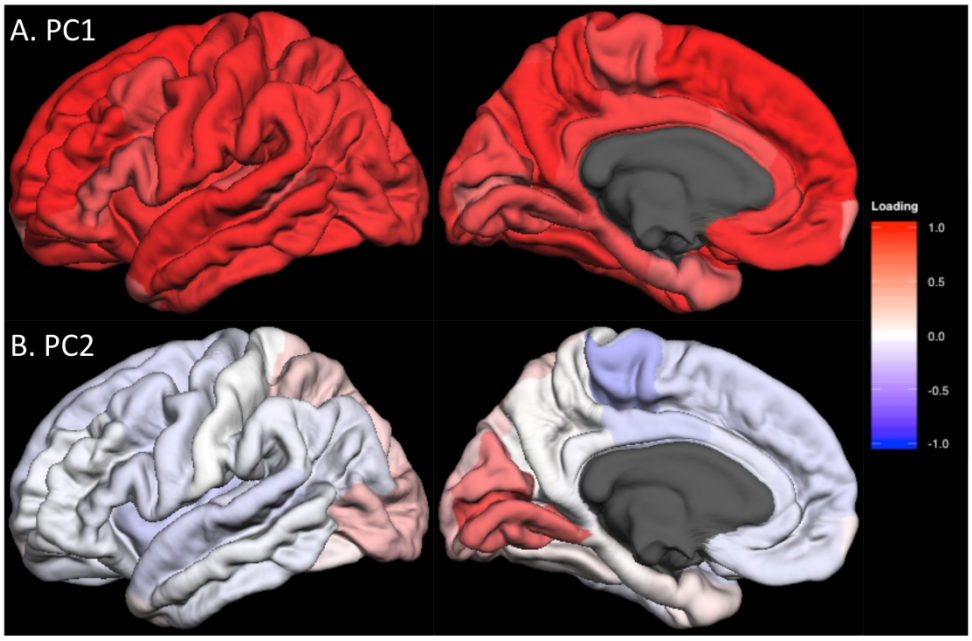
Figure 2. Genetic Loci of Global Variation of Cortical Surface Area. A, Manhattan plots of loci associated with PC1 of cortical surface area across the genome (upper panel), and in chromosome 17 (lower panel). The vertical axes represent the –log10 (p-values), and the horizontal axes represent the chromosome number (upper) or the hg19 position on chromosome 17 (lower). All the labeled genes indicate the protein-coding genes mapped to the GWAS-significant SNPs with p <5E-08 (indicated by the red-horizontal lines). Among these genes on chromosome 17, the red-colored genes *MAPT* and *IGF2BP1* have higher gene expression levels in the entire cerebral cortex during the prenatal period than the post-natal period (Figure 4). Regional association plots of the 42.9 – 47.3Mb region of chromosome 17 containing the GWAS-significant SNPs (panel **B**) and the three independent genetic loci (panel **C**) identified by FUMA(Watanabe et al. 2017). The horizontal axis indicates the genomic position on the human chromosome 17 (hg19). The left-vertical axis indicates the $-\log_{10}$ (p-values) obtained from the GWAS meta-analysis; and the right-vertical axis, the estimated recombination rate from the HapMap samples. The purple-colored index SNP indicates the top SNP (rs11652522, p = 1.6E-08) within the region (top panel), the top SNP within *MAPT* (rs62056789, p = 1.6E-19: middle panel) or *IGF2BP1* (rs11079849 p = 2.8E-10: bottom panel). The red-to-blue colors indicate the degree of linkage disequilibrium (LD) between each SNP and the index SNP. The LD was measured by the pairwise squared allelic correlation r^2 estimated in the 1000 Genomes European reference panels (Nov 2014 EUR). The plot was created using LocusZoom (http://locuszoom.org/).

Figure 3. Genetic Locus of Regional Variation of Cortical Surface Area (SA). A, Manhattan plot of loci associated with PC2 of surface area. The labelled gene on chromosome 14 is *DAAM1,* the protein-coding gene mapped to the GWAS-significant SNPs. *DAAM1* show high levels of expression in the entire cerebral cortex during the prenatal period (see Figure 4). **B,** Regional association plot for genomic locus containing *DAAM1*. The horizontal axis represents the genomic position on the human chromosome 14 (hg19). The left-vertical axis indicates the $-\log_{10}$ (p-values) obtained from the GWAS meta-analysis; and the right-vertical axis, the estimated recombination rate from the HapMap samples. The red-to-blue colors indicate the degree of linkage disequilibrium (LD) between each SNP and the top SNP (rs73313052, p = 2.4E-34). The LD was based on the pairwise squared allelic correlation r^2 estimated in the 1000 Genomes European reference panels (Nov 2014 EUR). The plot was created using LocusZoom (http://locuszoom.org/).

Figure 4. Spatial and temporal expression of genes mapped to GWAS-significant SNPs on chromosomes 17 (PC1) or 14 (PC2). A, Gene expression levels for the ten (chromosome 17) and the one (chromosome 14) protein coding genes measured by RMKM (reads per kilobase per million) as a function of human-brain developmental time. All the genes except for *DAAM1* are on chromosome 17. The time split into 9 windows based on post conception days (indicated by vertical dashed lines): 52-69 (window 1), 70-111 (window 2), 112-132 (window 3), 133-167 (window 4), 168-447 (window5), 448 - 1299 (window 6), 1300-4648 (window 7), 4649-7570 (window 8), and 7571-14876 (window 9). The boundary between pre- and postnatal periods is indicated by red vertical line. Each colored point represents the transformed expression level of each gene across 16 anatomical brain regions and ages. Brain structure includes 11 neocortical areas (NCX, blue), and 5 subcortical regions: hippocampus (HIP, cyan), amygdala (AMY, orange), striatum (STR, black), mediodorsal nucleus of thalamus (MD, dark green), and cerebellar cortex (CBC, red). **B,** Expression levels of the three 'developmental' genes *IGF2BP1*, *MPAT* and

DAAM1 that have higher expression (RPKM) in the 11 neocortical areas during prenatal (vs. postnatal) periods. The included neocortical regions are: orbitofrontal cortex (OFC, black), dorsolateral prefrontal cortex (DFC, blue), ventrolateral prefrontal cortex (VFC, purple), medial frontal cortex (MFC, magenta), primary motor cortex (M1C, red), primary sensory cortex (S1C, green), inferior parietal cortex (IPC, cyan), primary auditory cortex (A1C, grey), superior temporal cortex (STC, violet), inferior temporal cortex (ITC, yellow), primary visual cortex (V1C, brown).

Figure 5. Genetic correlations between PC1 and PC2 (surface area) and a number of complex traits related to general growth, brain function and several brain disorders. See Table E10 for the GWAS sources.



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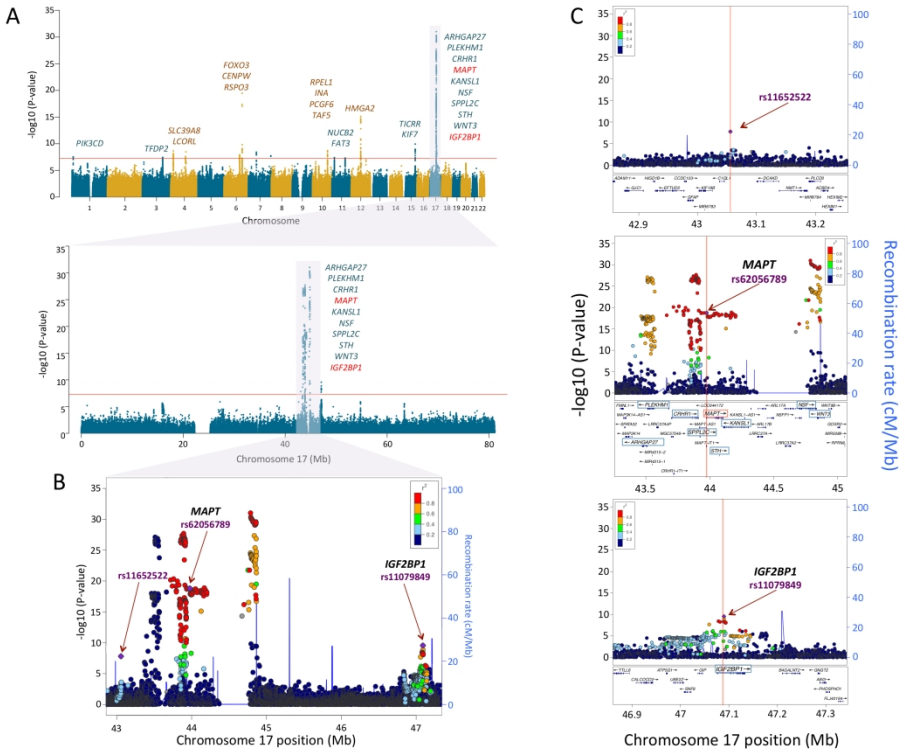

Figure 2

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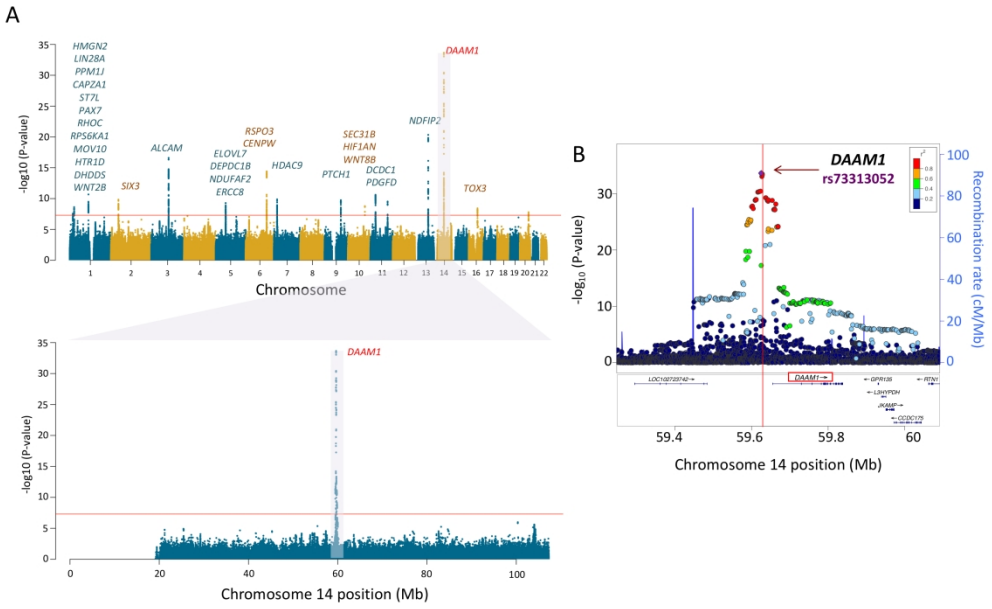

Figure 3

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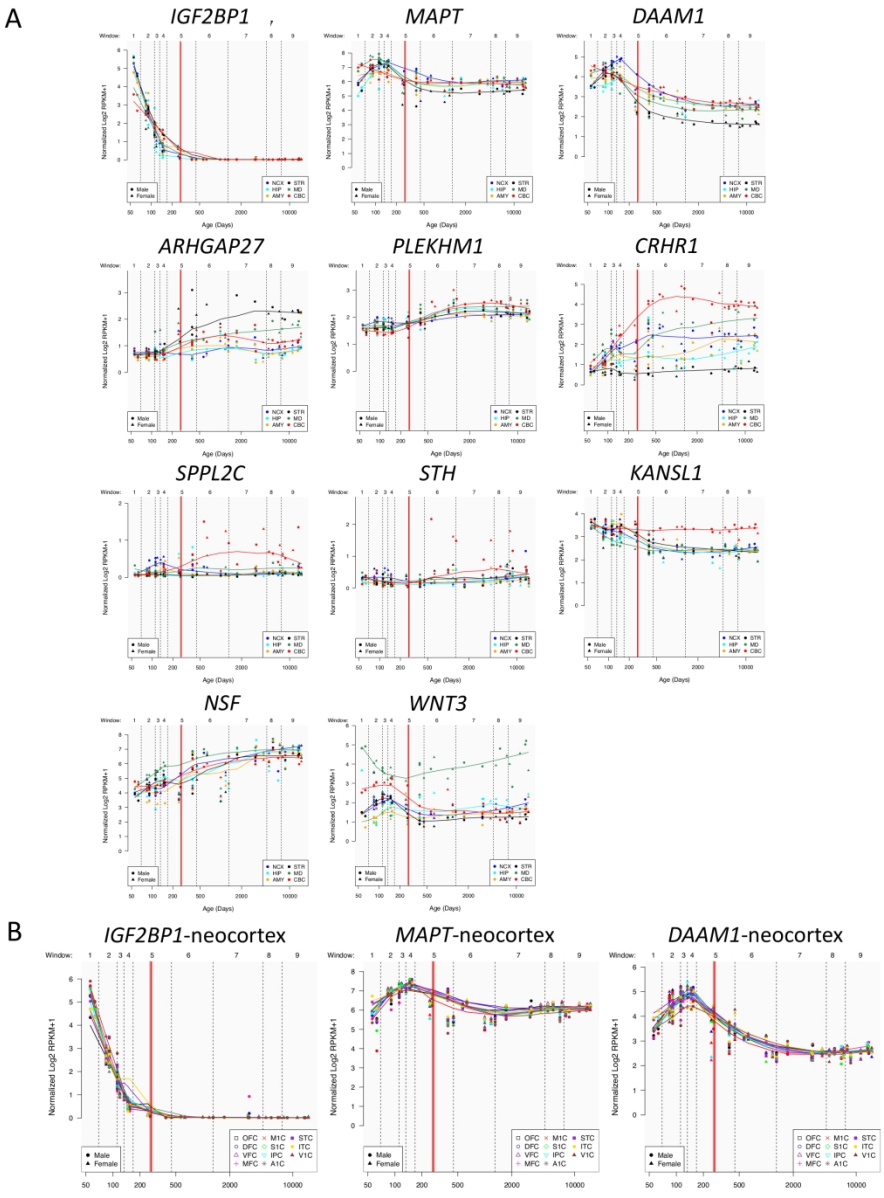

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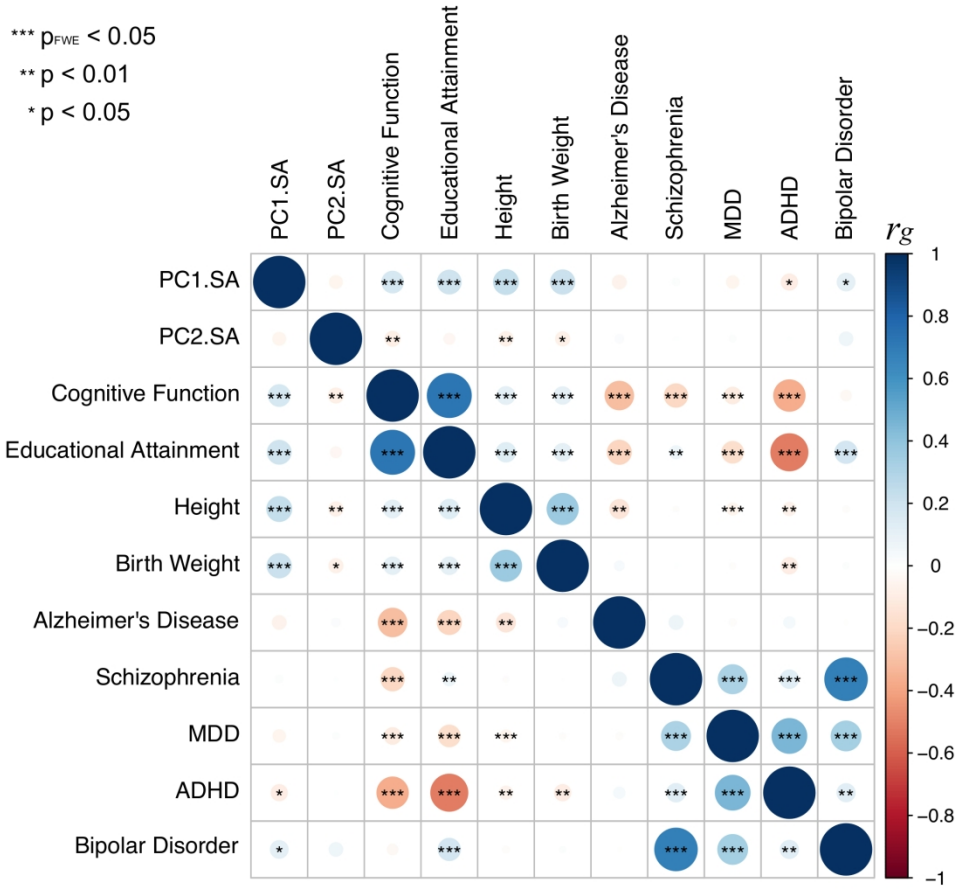

Figure 5. Genetic correlations between PC1 and PC2 (surface area) and a number of complex traits related to general growth, brain function and several brain disorders. See Table E10 for the GWAS sources.

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Shin J et al. Extended Data for "Global and regional development of the human cerebral cortex: molecular architecture and occupational aptitudes". *Cerebral Cortex* 2020

Extended Data Table Index

Table E1A. Demograpic information for the cohorts included in the meta-analyses of genome-wide association studies of surface area and cortical thickness principal component scores.

Cohort	Cohort Abbreviation	Study Design	Ancestry	Total N	Females N (%)	Age Range (years)
Atherosclerosis Risk in Communities Study	ARIC	Population-based	European	1,080	451 (42%)	45 - 64
Austrian Stroke Prevention Family Study	ASPSFam	Family-based	European	229	162 (71%)	38 - 86
BIL&GIN	BIL&GIN	Population-based	European	262	127 (48%)	18 - 57
Cardiovascular Health Study	CHS	Population-based	European	567	226 (40%)	73 - 95
Framingham Heart Study	FHS	Population-based	European	946	404 (43%)	34 - 85
LIFE-Adult	LIFE-Adult	Population-based	European	1,690	850 (50%)	20 - 82
Lothian Birth Cohort 1936	LBC1936	Population based	European	568	267 (47%)	70 - 74
Sydney Memory and Ageing Study	MAS	Population-based	European	376	236 (63%)	70 - 90
Older Australian Twin Study	OATS	Population based	European	280	203 (73%)	65 - 89
Rotterdam Study 1	RS1	Population-based	European	1,073	459 (43%)	69 - 96
Rotterdam Study 2	RS2	Population-based	European	1,148	551 (48%)	60 - 97
Rotterdam Study 3	RS3	Population-based	European	2,551	1,142 (45%)	45 - 89
Saguenay Youth Study - Adult	SYS-Adult	Family-based	European	515	241 (47%)	36 - 65
Saguenay Youth Study - Adolescent	SYS-Adolescent	Family-based	European	947	458 (48%)	12 - 18
Study of Health in Pomerania - 2	SHIP-2	Population based	European	1,073	557 (52%)	30 - 89
Study of Health in Pomerania - Trend1	SHIP-TREND1	Population based	European	857	482 (56%)	22 - 81
Study of Health in Pomerania - Trend2	SHIP-TREND2	Population based	European	1,076	529 (49%)	21 - 82
Three Cities-Dijon	3CDijon	Population-based	European	383	225 (58%)	65 - 83
UK Biobank	UKBB	Population-based	European	8,163	3,806 (47%)	48 - 63

Table E1B. Summary of brain imaging measures and acquisition parameters per cohort included in meta analyses of genome-wide association studies of surface area and cortical thickness principal component scores.

Cohort	Scanner(s)	Software	Citation(s) PMID	Acquistion Information
ARIC	1.5 T MRI scanners (General Electric Medical Systems)	FSL FIRST	2646917; 12090864	Total intracranial volume was measured from T1 weighted spin echo sagittal images, each set consisting of 32 contiguous 5 mm thick interleaved sections with no interslice gap, a field of view of 24 cm, and a matrix of 256 × 192, obtained with the following sequence: scan time, 2.5 minutes; echo time, 14 milliseconds; 2 repetitions; and repetition time, 500 milliseconds. A 3D volumetric spoiled gradient echo sequence with TR = 27 msec, TE = 9 msec, 124 contiguous partitions, 1.6 mm slice thickness, a 22 × 16.5 cm field of view, 192 views, and 45° flip angle was used to measure the volumes of the hippocampus and temporal horn. Interactive image processing steps were performed at the Mayo Clinic by a research associate who had no knowledge of the subjects' personal or medical histories
ASPSFam	MAGNETOM Trio, A Tim System, Siemens - Erlangen, Germany (3.0T)	Freesurfer v5.1	25309438	The conventional protocol included an axial FLAIR sequence (TR=10000ms, TE=69ms, inversion time=2500ms, num- ber of slices = 40, slice thickness = 3 mm, in-plane resolu- tion=0.86mm×0.86mm) and a high resolution T1 weighted 3D sequences with magnetization preparation (3D-MPRAGE) and whole brain coverage (TR=1900ms, TE=2.19ms, inversion time = 900 ms, flip angle = 9°, isotropic
BIL&GIN	3.0 T Tesla Philips ACHIVA scan ner (Philips Medical Systems, Best, The Netherlands)	FreeSurfer (5.3)	25840118	The acquisition protocol included a high resolution 3D T1-weighted sequence (3D-FFE-TFE; TR = 20 ms; TE = 4.6 ms; flip angle = 10°; inversion time = 800 ms; turbo field echo factor = 65; sense factor = 2; matrix size = 256 × 256 × 180 mm3; 1mm3 isotropic voxel size)
CHS	1.5 T MRI	FSL FIRST	21943959; 7847205; 8303738	MRI scanning was completed at each of the four sites using 1.5 Tesla scanners. The scanning protocol included a 3-D volumetric T1 weighted Spoiled Gradient Recall (SPGR) sequence covering the whole brain (TE/TR = 5/25, flip angle = 40°, NEX = 1, slice thickness = 1.5 mm/0 mm interslice gap), with an in-plane acquisition matrix of 256 × 256 × 124 image elements, 250 × 250 mm field of view and an in-plane voxel size of 0.98 mm3.
FHS	1 or 1.5 T Siemens Magnetom	FreeSurfer (5.3)	15653178	Subjects were imaged on a Siemens Magnetom(Munich, Germany), using a T2-weighted double spin-echo coronal imaging sequence of 4mm contiguous slices from nasion to occiput with a repetition time (TR) of 2420 ms, echo time (TE) of TE1 20/TE2 90 ms; echo train length 8 ms; field of view (FOV) 22 cm and an acquisition matrix of 182 × 256 interpolated to a 256 × 256 with one excitation.
LBC1936	GE Signa Horizon HDx 1.5 T	Freesurfer 5.3.0	14598854	fast 3-dimensional spoiled gradient-echo T1-weighted axial acquisition, with 2 excitations; 124 slices (1 mm thick)
LIFE	3T Siemens Verio scanner equipped with a 32 channel head coil	FreeSurfer (5.3)	26973099; 28397392	High resolution T1-weighted structural images were acquired using an MP-RAGE sequence with 1 mm isotropic voxels, 176 slices, TR=2300 ms, TE=2.98 ms, and inversion time (TI)=900 ms.
MAS	3T	Freesurfer 5.3	20637138	The 3D T1-weighted MRIs scans were used for computing the neuroimaging phenotypes and FreeSurfer v5.3 was used in the computation. T1-weighted scans had in-plane resoultion of 1 x 1 mm^2 and slice thickness = 1 mm with no gap in between, yielding 1 × 1 × 1 mm^3 isotropic voxels.
OATS	1.5T and 3T	Freesurfer 5.3		The 3D T1-weighted MRIs scans were used for computing the neuroimaging phenotypes. The sequence was performed using a similar protocol for the 1.5 Tesla scanners in the three centres with in-plane resolution = 1 × 1 mm, slice thickness = 1.5 mm, slice number = 144. The acquisition parameters for the 3 Tesla Philips scanner in centre 1 in-plane resolution = 1 × 1 mm, slice thickness = 1 mm, slice number = 190, resulting isotropic voxels of 1 × 1 × 1 mm^3.
RS2,RS2,RS3	1.5 T MRI unit (GE Healthcare, Milwaukee, USA, software version 11×)	FreeSurfer (4.5)	22002080	Structural imaging is performed with T1-weighted (T1w), proton density-weighted (PDw) and fluid-attenuated inversion recovery (FLAIR) sequences. The combination of different MR contrasts provided by these sequences can be used for automated brain tissue and white matter lesion segmentation (see section on processing). For this purpose, the T1w scan is acquired in 3D at high in-plane resolution and with thin slices (voxel size <1 mm3).
SHIP	Magnetom Avanto, Siemens Medical Systems, Erlangen, Germany, 1.5 Tesla	Freesurfer 5.3	20167617	T1-weighted magnetization prepared rapid acquisition gradient echo (MPRAGE) sequence
SHIP-Trend	Magnetom Avanto, Siemens Medical Systems, Erlangen, Germany, 1.5 Tesla	Freesurfer 5.3	20167617	T1-weighted magnetization prepared rapid acquisition gradient echo (MPRAGE) sequence
SYS-Adult	1.5 T Siemens (Avanto) scanner	FreeSurfer	25454417	T1W, 1-mm, isotropic resolution images acquired with a 3D fast radio frequency (RF)-spoiled gradient-echo scan.
SYS-Adolescent	1.0 T Philips	FreeSurfer (5.1.0)	17469173	Three-dimensional (3D) radio frequency (RF)-spoiled gradient-echo scan with 140 –160 slices, an isotropic resolution of 1 mm, a repetition time (TR) of 25 ms, an echo time (TE) of 5 ms, and flip angle of 30°
3CDijon	SIEMENS Magnetom (1.5T)	Freesurfer 5.3.0	14598854, 17977521	3D IR-FSPGR (T1); 2D FSE
UKBB	3.0 T Siemens Skyra running VD13A SP4, with a standard Siemens 32-channel RF receive head coil	FreeSurfer	27643430	T1W, acquired in the sagittal plane using a 3D magnetization-prepared rapid gradient-echo sequence at a resolution of 1×1×1 mm, with a 208×256×256 field of view

Table E1C. Genotyping, quality control, imputation and GWAS analysis software

Cohort	Genotyping Platform	Sample and variant quality control	Phasing/Imputation software	Reference Panel	Association Software (version)
ARIC	Affymetrix SNP Array 6.0	Sample callrate ≥ 95%, MAF > 0.01 & Rsq > 0.3, 0.005 < MAF <= 0.01 & Rsq > 0.8	SHAPEIT (v1.r532)/IMPUTE2	1000 Genomes phase 1 version 3	ProbABEL
ASPS	Illumina Human610-Quad BeadChip	Sample call rate 98%, SNP call rate 98%, MAF 0.01, HWE-pvalue 1×10-6, Other sample exclusions: Non-European ancestry, sample failures, sex mismatch, high autosomal heterozygosity, cryptic relatedness	SHAPEIT (v1.r790)/IMPUTE2 (v2.3.1)	1000 Genomes ALL phase 1 version 3	Plink
BIL&GIN	Illumina InfiniumOmniExpressExome-8v1-4	MAF 1%, SNP call rate 95%, sample call rate 95%, HWE p-value 10^{-6}, sample failures, sex mismatch, cryptic relatedness, ancestry outliers (smartPCA)	mach (v1.0.18)/Minimac3 (v2.0.1)	1000G EUR v3 (http://enigma.ini.usc.edu/wp-content/uploads/2012/07/v3.20101123.ENIGMA2.EUR.20120719.vcf.tgz)	Plink (v1.90b3w)
CHS-EA	Illumina 370 CNV, ITMAT-Broad-CARe (IBC)	For SNPs, the following exclusions were applied : Call rate < 97%, HWE P < 10-5, > 2 duplicate errors or Mendelian inconsistencies (for reference CEPH trios), heterozygote frequency = 0, SNP not found in HapMap.	MaCH + minimac (release stamp 2012-11-16)	1000 Genomes phase 1 version 3	R
FHS	Affymetrix GeneChip Human Mapping 500K Array Set® and 50K Human Gene Focused Panel®	Sample Level QC: sample call rate ≥ 97%, sample failures, genotyped sex different from recorded sex, discordance based on pedigree analyses; SNP level QC: SNP call rate ≥ 97%, a deviation from Hardy-Weinberg (HWE) ≥ 1x10-6, Mendel errors ≤ 1000, and MAF ≥ 1%, on chromosome 1-22, or X with a physical location on Build 37.	MaCH/minimac	1000 Genomes phase 1 version 3	GWAF
LBC1936	Illumina Human 610_Quadv1	MAF>1%, SNP call rate >0.98, sample call rate >0.95, HWE p-value 10^{-3}, Non-European ancestry not included	minimac/minimac	1000G Phase I Version III with All ethnicities (2010-11 data freeze, 2012-03-14 haplotypes)	HASE
LIFE-Adult	Affymetrix Axiom CEU1 SNP array	Sample quality filters were dish-QC<0.82, call rate<97%, heterozygosity outliers, sex-mismatch, cryptic relatedness and outliers of principal components analysis (>6SD of first 10 PCs). SNP quality filters were call rate<97%, cluster plot irregularities as recommended by Affymetrix, p-value of exact Hardy-Weinberg equilibrium test <1e-6 and p-value of plate association <1e-7.	SHAPEIT (v2.r790)/ IMPUTE2 (v2.3.2)	1kG phase 1, version 3 (2012)	PLINK 1.9
MAS	Affymetrix Genome-wide Human SNP Array 6.0	MAF 1%, HWE p-value 10^{-6}, SNP call rate 98%, sample call rate 95%, Sex, relatedness and assesment of population stratification	MaCH/minimac	1000 Genomes phase 1 version 3	mach2qtl
OATS	Illumina Omniexpress	MAF 1%, HWE p-value 10^{-6}, SNP call rate 98%, sample call rate 95%, Sex, relatedness and assesment of population stratification	MaCH/minimac	1000 Genomes phase 1 version 3	merlin
RS1	Illumina 550 (+duo), Illumina 610 quad	SNP call rate 98%, MAF 0.01, HWE p-value 10^{-6}	MaCH/minimac	1000 Genomes phase 1 version 3	HASE
RS2	Illumina 550 duo	SNP call rate 98%, MAF 0.01, HWE p-value 10^{-6}	MaCH/minimac	1000 Genomes phase 1 version 3	HASE
RS3	Illumina 610 quad	SNP call rate 98%, MAF 0.01, HWE p-value 10^{-6}	MaCH/minimac	1000 Genomes phase 1 version 3	HASE
SYS	Illumina Human610W-Quad Beadchip (Quad), Illumina HumanOmniExpress BeadChip (Omni)	MAF>1%, call rate >0.95 per chip, HWE p-value <10e-6	SHAPEIT/IMPUTE2	1000 Genomes release March 2012 (EUR reference panel)	GenABEL/ProbABEL
3CDijon	Illumina Human 610 Quad BeadChip®	SNP call rate 95%, sample call rate 98%, HWE p-value 10^{-6}, MAF 0.01, discordance between genotyped and recorded sex, excess inter/intra heterozygosity, non-European ancestry	MiniMac RELEASE STAMP 2012-11-16	1000G (phase-1, version-3)	HASE
SHIP	Affymetrix SNP 6.0	HWE p-value 10^{-4}, call rate 80%, sample call rate 92%, duplicate samples (by IBS) or reported/genotyped gender mismatch	IMPUTE2 v2.2.2	ALL 1000 Genomes (phase 1 version 3; March 2012)	QUICKTEST v0.95
SHIP-Trend	Illumina Omni 2.5	HWE p-value 10^{-4}, call rate 90%, sample call rate 94%, duplicate samples (by IBS) or reported/genotyped gender mismatch	IMPUTE2 v2.2.2	ALL 1000 Genomes (phase 1 version 3; March 2012)	QUICKTEST v0.95
UKBB	Applied Biosystems™ UK BiLEVE Axiom™ Array by Affymetrix and Applied Biosystems™ UK Biobank Axiom™ Array	HWE p-value 10^{-6}, call rate 95%, sample call rate 95%, non-European ancestry, sample failures, sex mismatch, high autosomal heterozygosity, cryptic relatedness	SHPAEIT (v3)/IMPUTE4	Haplotype Reference Consortium (HRC, version 1.1)	HASE

Table E2. Median PC-loading values for surface area and thickness measurements in 34 cortical regions across the following cohorts: ARIC, ASPSFam, BIL&GIN, CHS, FHS, LIFE-Adult, RS, SPS and SYS. The median loading values were then used to derive the 'general' PC score for each individual and later used as the response variable in the meta-GWAS analyses. Cohort abbreviations are presented in Table E1A.

	Surface area		Thickness	
roi	**PC1**	**PC2**	**PC1**	**PC2**
bankssts	0.6839	-0.1259	0.7080	-0.0943
caudalanteriorcingulate	0.6655	-0.0775	0.2974	0.4473
caudalmiddlefrontal	0.7222	-0.1077	0.7784	-0.1604
cuneus	0.7101	0.4596	0.5934	-0.3457
entorhinal	0.5385	0.0748	0.3627	0.2540
fusiform	0.8226	0.0618	0.7682	0.0808
inferiorparietal	0.7884	-0.0768	0.8343	-0.2348
inferiortemporal	0.7974	-0.0703	0.7441	0.1809
isthmuscingulate	0.7447	-0.0212	0.4923	0.2233
lateraloccipital	0.7837	0.2434	0.7255	-0.2518
lateralorbitofrontal	0.8246	-0.0738	0.6591	0.3972
lingual	0.6825	0.5413	0.6841	-0.1453
medialorbitofrontal	0.8213	-0.0818	0.5140	0.4537
middletemporal	0.8372	-0.0364	0.8170	0.1122
parahippocampal	0.6664	0.0215	0.3596	0.2147
paracentral	0.7042	-0.2791	0.7225	-0.2283
parsopercularis	0.6559	-0.0950	0.7730	0.0548
parsorbitalis	0.7591	-0.0407	0.6611	0.2047
parstriangularis	0.6359	-0.0740	0.7505	0.1017
pericalcarine	0.5362	0.6727	0.5166	-0.3158
postcentral	0.8276	-0.0041	0.7430	-0.3004
posteriorcingulate	0.7426	-0.1489	0.5791	0.3150
precentral	0.8176	-0.0900	0.7967	-0.2481
precuneus	0.8406	0.0102	0.8101	-0.1645
rostralanteriorcingulate	0.7602	-0.0888	0.3563	0.5776
rostralmiddlefrontal	0.8632	-0.0364	0.7828	0.0806
superiorfrontal	0.8854	-0.1109	0.8432	-0.0042
superiorparietal	0.7767	0.1563	0.7963	-0.3984
superiortemporal	0.8544	-0.1201	0.8069	0.0146
supramarginal	0.8076	-0.0528	0.8669	-0.1625
frontalpole	0.4631	0.0541	0.5000	0.2030
temporalpole	0.5783	0.0894	0.4787	0.2271
transversetemporal	0.6562	-0.0924	0.6340	-0.1050
insula	0.7925	-0.1725	0.6321	0.3228

Table E3.Genomic loci with independent significant SNPs identified in meta analyses of GWAS of surface area-PC1 and -PC2, obtained by FUMA[1]

PC domension	Ind. SNP No	Genomic Locus	Genomic Locus start	Genomic Locus end	chr	pos	uniqID	rsID	p	nSNPs	nGWASSNPs
1	1	1	9720496	9721289	1	9720526	1:9720526:A:G	rs58784124	2.854E-08	5	5
1	2	2	141637438	141847759	3	141720712	3:141720712:A:G	rs34186890	3.596E-08	115	95
1	3	3	17792249	18035250	4	17924734	4:17924734:C:T	rs11938781	2.244E-09	253	215
1	4	4	103001649	103387161	4	103188709	4:103188709:C:T	rs13107325	4.473E-08	5	5
1	5	4	103001649	103387161	4	103292422	4:103292422:C:T	rs13109272	2.458E-08	19	14
1	6	5	106009763	106009763	4	106009763	4:106009763:A:G	rs2301718	3.319E-09	1	1
1	7	6	108861264	109019323	6	108977663	6:108977663:C:T	rs9400239	1.172E-08	65	60
1	8	6	108861264	109019323	6	108995187	6:108995187:A:G	rs61192764	1.442E-08	12	9
1	9	7	126648460	127369230	6	126704795	6:126704795:C:T	rs9388490	1.953E-09	246	202
1	10	7	126648460	127369230	6	126792095	6:126792095:A:G	rs11759026	3.584E-20	4	4
1	11	7	126648460	127369230	6	126986996	6:126986996:A:G	rs1262476	8.103E-10	22	19
1	12	7	126648460	127369230	6	127204623	6:127204623:A:G	rs9375477	1.567E-10	3	2
1	13	7	126648460	127369230	6	127369230	6:127369230:C:T	rs139849708	4.531E-09	13	13
1	14	8	54909928	55015505	7	54966738	7:54966738:A:G	rs77126132	3.776E-09	24	24
1	15	9	155772027	155778152	7	155778152	7:155778152:A:G	rs75745313	1.797E-08	2	2
1	16	10	104591182	105175131	10	105012994	10:105012994:C:T	rs1628768	1.993E-09	45	38
1	17	11	17067849	17365209	11	17310391	11:17310391:C:T	rs55948574	3.959E-08	74	59
1	18	12	92317858	92558342	11	92355990	11:92355990:A:T	rs3911562	4.832E-08	85	67
1	19	13	66257355	66389968	12	66306441	12:66306441:A:C	rs12298541	1.995E-08	2	1
1	20	13	66257355	66389968	12	66325689	12:66325689:C:T	rs343086	2.534E-09	1	1
1	21	13	66257355	66389968	12	66367726	12:66367726:C:T	rs61921611	5.671E-10	5	3
1	22	13	66257355	66389968	12	66376091	12:66376091:C:T	rs7306710	7.556E-16	23	21
1	23	13	66257355	66389968	12	66386396	12:66386396:C:T	rs11175990	4.152E-08	6	6
1	24	13	66257355	66389968	12	66387621	12:66387621:A:T	rs10748027	4.565E-08	1	1
1	25	13	66257355	66389968	12	66389968	12:66389968:C:T	rs10400419	2.086E-11	4	3
1	26	14	68216239	68225876	12	68216239	12:68216239:A:T	rs35227403	2.306E-08	2	2
1	27	15	90081905	90208310	15	90081905	15:90081905:A:G	rs28792763	1.721E-08	58	53
1	28	15	90081905	90208310	15	90128223	15:90128223:A:C	rs893725	1.153E-10	144	122
1	29	16	43055579	43055579	17	43055579	17:43055579:A:C	rs11652522	1.585E-08	1	1
1	30	17	43399058	44874453	17	43399058	17:43399058:C:G	rs117642368	8.939E-12	2	2
1	31	17	43399058	44874453	17	43460891	17:43460891:A:G	rs61572747	2.479E-14	1	1
1	32	17	43399058	44874453	17	43512318	17:43512318:A:G	rs56168933	7.662E-28	3241	475
1	33	17	43399058	44874453	17	43798308	17:43798308:A:G	rs117615688	4.427E-08	2	1
1	34	17	43399058	44874453	17	43871147	17:43871147:A:G	rs12944712	4.993E-11	20	20
1	35	17	43399058	44874453	17	43901074	17:43901074:A:G	rs173365	3.538E-10	8	8
1	36	17	43399058	44874453	17	43915497	17:43915497:C:T	rs62054807	2.118E-11	2935	336
1	37	17	43399058	44874453	17	43992943	17:43992943:A:G	rs9899833	5.179E-09	9	1
1	38	17	43399058	44874453	17	44787312	17:44787312:C:T	rs1378358	9.548E-32	3102	409
1	39	17	43399058	44874453	17	44793283	17:44793283:C:T	rs17692129	1.529E-10	4	3
1	40	17	43399058	44874453	17	44865439	17:44865439:G:T	rs2074404	1.957E-17	1840	241
1	41	17	43399058	44874453	17	44866602	17:44866602:C:T	rs199497	3.822E-10	2	2
1	42	18	47060322	47145848	17	47090785	17:47090785:C:T	rs11079849	2.803E-10	36	30
2	43	19	18956404	18992466	1	18962095	1:18962095:C:T	rs1934057	2.776E-08	26	23
2	44	20	23473592	23543929	1	23541078	1:23541078:A:T	rs7519093	3.028E-08	6	5
2	45	21	26752992	26902694	1	26752992	1:26752992:C:T	rs4659441	2.43E-09	25	22
2	46	21	26752992	26902694	1	26900805	1:26900805:A:G	rs12121702	2.428E-08	28	25
2	47	22	113054659	113252614	1	113054659	1:113054659:C:T	rs351370	1.936E-08	1	1
2	48	22	113054659	113252614	1	113063125	1:113063125:A:G	rs910697	3.26E-10	70	57
2	49	22	113054659	113252614	1	113239478	1:113239478:C:T	rs2999158	2.132E-11	4	4
2	50	22	113054659	113252614	1	113248365	1:113248365:A:G	rs954679	4.384E-10	5	5

PC domension	Ind. SNP No	Genomic Locus	Genomic Locus start	Genomic Locus end	chr	pos	uniqID	rsID	p	nSNPs	nGWASSNPs
2	51	23	45130410	45175585	2	45138444	2:45138444:A:C	rs540395	3.796E-08	10	10
2	52	23	45130410	45175585	2	45167570	2:45167570:G:T	rs83995	1.492E-10	24	24
2	53	24	104646815	104828166	3	104658328	3:104658328:C:T	rs6783013	9.705E-10	52	43
2	54	24	104646815	104828166	3	104660608	3:104660608:C:G	rs13077489	4.577E-08	2	2
2	55	24	104646815	104828166	3	104669023	3:104669023:G:T	rs6789712	1.236E-08	72	67
2	56	24	104646815	104828166	3	104683753	3:104683753:C:T	rs9288795	1.715E-15	224	208
2	57	24	104646815	104828166	3	104724787	3:104724787:A:T	rs971550	2.537E-17	49	42
2	58	24	104646815	104828166	3	104738751	3:104738751:A:G	rs6437556	1.381E-10	103	93
2	59	24	104646815	104828166	3	104823350	3:104823350:A:G	rs2399023	9.739E-09	67	63
2	60	25	59823118	60465365	5	60030791	5:60030791:A:T	rs7381195	5.274E-10	62	57
2	61	25	59823118	60465365	5	60069057	5:60069057:C:T	rs13158665	3.201E-09	39	34
2	62	25	59823118	60465365	5	60139881	5:60139881:A:G	rs62372102	1.433E-09	178	148
2	63	26	126525715	127369230	6	126613946	6:126613946:C:T	rs76470478	3.427E-09	4	1
2	64	26	126525715	127369230	6	126717064	6:126717064:A:G	rs1591805	2.012E-09	240	200
2	65	26	126525715	127369230	6	126745633	6:126745633:A:C	rs139214174	2.38E-11	14	13
2	66	26	126525715	127369230	6	127083941	6:127083941:C:T	rs9385403	3.946E-15	24	23
2	67	27	18869552	18933411	7	18904400	7:18904400:C:G	rs12700001	1.329E-10	49	47
2	68	28	98147278	98279801	9	98147804	9:98147804:C:T	rs7860361	1.34E-08	19	17
2	69	28	98147278	98279801	9	98192383	9:98192383:A:T	rs28710957	1.823E-08	3	3
2	70	28	98147278	98279801	9	98213728	9:98213728:C:G	rs9632916	1.825E-10	36	29
2	71	29	102245664	102371946	10	102245664	10:102245664:C:T	rs149658356	4.852E-08	2	2
2	72	29	102245664	102371946	10	102366639	10:102366639:C:T	rs138740906	1.702E-09	4	3
2	73	30	30798255	31020084	11	30861472	11:30861472:C:G	rs808471	2.446E-11	160	139
2	74	30	30798255	31020084	11	31010455	11:31010455:A:G	rs9667150	2.175E-08	134	118
2	75	31	103985306	104041862	11	104012656	11:104012656:A:G	rs1681464	3.021E-10	31	26
2	76	32	79859456	80251200	13	80162555	13:80162555:C:T	rs9545142	2.388E-08	109	85
2	77	32	79859456	80251200	13	80182535	13:80182535:A:T	rs9545151	3.696E-12	13	12
2	78	32	79859456	80251200	13	80188702	13:80188702:C:T	rs9601250	1.705E-13	2	2
2	79	32	79859456	80251200	13	80191817	13:80191817:C:G	rs9545154	4.616E-21	26	23
2	79	32	79859456	80251200	13	80191817	13:80191817:C:G	rs9545154	4.616E-21	26	23
2	80	32	79859456	80251200	13	80236762	13:80236762:A:G	rs9318650	3.425E-13	44	40
2	81	33	59449138	59891607	14	59466003	14:59466003:A:G	rs79329625	5.735E-12	104	96
2	82	33	59449138	59891607	14	59577898	14:59577898:C:T	rs78570253	6.214E-15	96	88
2	83	33	59449138	59891607	14	59585932	14:59585932:A:C	rs4898978	1.746E-20	14	13
2	84	33	59449138	59891607	14	59609282	14:59609282:G:T	rs4258526	5.34E-10	3	3
2	85	33	59449138	59891607	14	59622767	14:59622767:A:C	rs76119478	9.026E-09	2	2
2	86	33	59449138	59891607	14	59625980	14:59625980:A:G	rs11158250	5.574E-18	2	1
2	87	33	59449138	59891607	14	59625997	14:59625997:A:G	rs73313052	2.363E-34	50	43
2	88	33	59449138	59891607	14	59629611	14:59629611:G:T	rs2053300	2.516E-08	2	2
2	89	33	59449138	59891607	14	59633677	14:59633677:A:G	rs4898980	4.463E-08	2	2
2	90	33	59449138	59891607	14	59648738	14:59648738:C:T	rs893516	1.064E-21	3	2
2	91	33	59449138	59891607	14	59664984	14:59664984:C:T	rs1252916	3.016E-08	2	2
2	92	33	59449138	59891607	14	59665934	14:59665934:C:T	rs8016570	1.022E-11	15	12
2	93	33	59449138	59891607	14	59683086	14:59683086:C:T	rs78445564	1.129E-10	4	4
2	94	33	59449138	59891607	14	59684859	14:59684859:A:G	rs74874233	4.449E-14	126	116
2	95	33	59449138	59891607	14	59694643	14:59694643:A:G	rs2757117	3.892E-10	1	1
2	96	33	59449138	59891607	14	59801714	14:59801714:A:G	rs61984497	3.18E-09	89	83
2	97	33	59449138	59891607	14	59815097	14:59815097:A:G	rs61984499	8.887E-10	150	131
2	98	34	52538040	52635000	16	52585440	16:52585440:C:T	rs3112578	3.841E-09	29	25
2	99	35	52448936	52471667	20	52466100	20:52466100:C:T	rs10432728	1.648E-08	29	19

[1]K. Watanabe, E. Taskesen, A. van Bochoven and D. Posthuma. Functional mapping and annotation of genetic associations with FUMA. Nat. Commun. 8:1826. (2017)

Table E4A. GWAS meta-analysis results for surface area PC1 for SNPs with p <5E-08.

The table shows the genomic positions, alleles,mapped genes, and the functions with respect to the mapped genes. The association results are from the meta-GWAS; UKBB and ENIGMA cohorts.

											Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			
rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	Replicated**
rs58380009	1	9720496	1	9720496	9721289	T	C	0.2197	PIK3CD	intronic	0.9904	0.1791	3.19E-08	0.3613	0.3344	2.80E-01	0.0126	0.0130	3.29E-01	0
rs58784124	1	9720526	1	9720496	9721289	A	G	0.2217	PIK3CD	intronic	-0.9938	0.1791	2.85E-08	-0.3588	0.3343	2.83E-01	-0.0123	0.0130	3.43E-01	0
rs12088060	1	9721289	1	9720496	9721289	A	G	0.2217	PIK3CD:RP11-558F	ncRNA_intronic	0.9924	0.1796	3.29E-08	0.3655	0.3342	2.74E-01	0.0128	0.0130	3.24E-01	0
rs12495978	3	141707113	2	141637438	141847759	T	G	0.1779	TFDP2	intronic	-1.0453	0.1912	4.60E-08	-1.5674	0.3751	2.97E-05	-0.0917	0.0139	4.52E-11	1
rs1511299	3	141716072	2	141637438	141847759	T	C	0.2604	TFDP2	intronic	-0.8564	0.1557	3.80E-08	-0.8673	0.3064	4.66E-03	-0.0506	0.0112	6.11E-06	1
rs34186890	3	141720712	2	141637438	141847759	A	G	0.2614	TFDP2	intronic	-0.8576	0.1556	3.60E-08	-0.8742	0.3061	4.30E-03	-0.0506	0.0112	6.16E-06	1
rs7671110	4	17874089	3	17792249	18035250	T	C	0.1252	LCORL	intronic	-1.0865	0.1914	1.37E-08	-1.1556	0.3683	1.71E-03	-0.0389	0.0138	4.86E-03	1
rs7663887	4	17902920	3	17792249	18035250	A	C	0.1252	LCORL	intronic	-1.0873	0.1912	1.29E-08	-1.1351	0.3671	2.00E-03	-0.0378	0.0138	6.15E-03	1
rs13138182	4	17908413	3	17792249	18035250	A	G	0.1252	LCORL	intronic	1.0899	0.1912	1.20E-08	1.1334	0.3671	2.03E-03	0.0376	0.0138	6.36E-03	1
rs1472852	4	17910236	3	17792249	18035250	A	C	0.1252	LCORL	intronic	-1.0859	0.1911	1.33E-08	-1.1490	0.3673	1.77E-03	-0.0373	0.0138	6.70E-03	1
rs6813340	4	17922866	3	17792249	18035250	A	G	0.1252	LCORL	intronic	1.0945	0.1911	1.03E-08	1.1242	0.3678	2.25E-03	0.0372	0.0137	6.75E-03	1
rs11938781	4	17924734	3	17792249	18035250	T	C	0.1451	LCORL	intronic	1.1313	0.1892	2.24E-09	1.1246	0.3647	2.05E-03	0.0416	0.0138	2.49E-03	1
rs13146142	4	17931318	3	17792249	18035250	T	C	0.1262	LCORL	intronic	1.0933	0.1907	9.81E-09	1.1187	0.3673	2.33E-03	0.0359	0.0137	8.56E-03	1
rs73802707	4	17932319	3	17792249	18035250	T	C	0.1193	LCORL	intronic	-1.1240	0.1955	8.98E-09	-1.0215	0.3721	6.07E-03	-0.0360	0.0143	1.16E-02	1
rs6841793	4	17933810	3	17792249	18035250	C	G	0.1262	LCORL	intronic	1.0820	0.1904	1.32E-08	1.1337	0.3671	2.02E-03	0.0361	0.0136	8.06E-03	1
rs6449345	4	17934394	3	17792249	18035250	A	T	0.1262	LCORL	intronic	1.0804	0.1904	1.39E-08	1.1330	0.3672	2.04E-03	0.0362	0.0136	8.04E-03	1
rs6449346	4	17934461	3	17792249	18035250	T	C	0.1262	LCORL	intronic	1.0784	0.1903	1.46E-08	1.1343	0.3671	2.01E-03	0.0361	0.0136	8.05E-03	1
rs7663818	4	17936443	3	17792249	18035250	T	C	0.1262	LCORL	intronic	-1.0620	0.1903	2.38E-08	-1.1370	0.3671	1.96E-03	-0.0360	0.0136	8.23E-03	1
rs7692995	4	17936634	3	17792249	18035250	T	C	0.1262	LCORL	intronic	1.0755	0.1903	1.59E-08	1.1371	0.3671	1.96E-03	0.0360	0.0136	8.25E-03	1
rs34683079	4	17939302	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0795	0.1901	1.36E-08	1.1363	0.3671	1.97E-03	0.0355	0.0136	9.14E-03	1
rs6840868	4	17939331	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0794	0.1901	1.37E-08	-1.1367	0.3671	1.97E-03	-0.0354	0.0136	9.17E-03	1
rs6845118	4	17939740	3	17792249	18035250	T	G	0.1272	LCORL	intronic	-1.1009	0.1911	8.33E-09	-1.1363	0.3671	1.97E-03	-0.0362	0.0138	8.59E-03	1
rs12511600	4	17939921	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0801	0.1901	1.33E-08	-1.1364	0.3671	1.97E-03	-0.0355	0.0136	9.14E-03	1
rs71603391	4	17940197	3	17792249	18035250	A	G	0.1282	LCORL	intronic	1.1222	0.1937	6.84E-09	1.1297	0.3670	2.09E-03	0.0357	0.0141	1.13E-02	1
rs73098845	4	17940718	3	17792249	18035250	A	C	0.1272	LCORL	intronic	-1.0778	0.1901	1.44E-08	-1.1357	0.3672	1.99E-03	-0.0354	0.0136	9.24E-03	1
rs73098848	4	17941027	3	17792249	18035250	C	G	0.1272	LCORL	intronic	-1.0782	0.1901	1.42E-08	-1.1359	0.3672	1.99E-03	-0.0354	0.0136	9.28E-03	1
rs16896068	4	17944840	3	17792249	18035250	A	G	0.1282	LCORL	intronic	-1.0815	0.19	1.25E-08	-1.1366	0.3675	1.99E-03	-0.0353	0.0136	9.42E-03	1
rs16896074	4	17947873	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0677	0.1899	1.87E-08	1.1663	0.3666	1.47E-03	0.0347	0.0136	1.05E-02	1
rs12503997	4	17948089	3	17792249	18035250	A	T	0.1272	LCORL	intronic	-1.0726	0.1898	1.60E-08	-1.1665	0.3665	1.46E-03	-0.0347	0.0136	1.06E-02	1
rs12506752	4	17948352	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0710	0.1898	1.68E-08	-1.1665	0.3665	1.46E-03	-0.0346	0.0136	1.07E-02	1
rs11936915	4	17948497	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0710	0.1898	1.69E-08	1.1665	0.3665	1.46E-03	0.0346	0.0136	1.07E-02	1
rs11936911	4	17948668	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0727	0.1898	1.59E-08	1.1666	0.3665	1.46E-03	0.0346	0.0136	1.07E-02	1
rs6850259	4	17949607	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0691	0.1899	1.80E-08	1.1656	0.3667	1.49E-03	0.0346	0.0136	1.08E-02	1
rs34934312	4	17950172	3	17792249	18035250	A	T	0.1272	LCORL	intronic	-1.0668	0.19	1.95E-08	-1.1394	0.3676	1.95E-03	-0.0345	0.0136	1.09E-02	1
rs16896101	4	17950626	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0670	0.19	1.95E-08	1.1394	0.3676	1.95E-03	0.0345	0.0136	1.10E-02	1
rs16896113	4	17950850	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0721	0.1899	1.64E-08	1.1391	0.3676	1.95E-03	0.0355	0.0136	8.92E-03	1
rs7657678	4	17951035	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0670	0.19	1.95E-08	1.1392	0.3676	1.95E-03	0.0344	0.0136	1.13E-02	1
rs6843330	4	17952056	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0671	0.19	1.94E-08	-1.1393	0.3676	1.95E-03	-0.0342	0.0136	1.16E-02	1
rs6449349	4	17952609	3	17792249	18035250	C	G	0.1272	LCORL	intronic	-1.0693	0.1899	1.80E-08	-1.1645	0.3667	1.50E-03	-0.0341	0.0136	1.20E-02	1
rs7675806	4	17952959	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0704	0.1899	1.74E-08	1.1655	0.3666	1.48E-03	0.0342	0.0136	1.18E-02	1
rs16896128	4	17953590	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0713	0.1899	1.68E-08	1.1655	0.3666	1.48E-03	0.0341	0.0136	1.20E-02	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs7660642	4	17956017	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0686	0.1899	1.82E-08	1.1578	0.3667	1.60E-03	0.0340	0.0136	1.21E-02	1
rs4642247	4	17957158	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0674	0.19	1.94E-08	-1.1387	0.3676	1.96E-03	-0.0338	0.0136	1.26E-02	1
rs4057984	4	17957200	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0674	0.19	1.94E-08	1.1387	0.3676	1.96E-03	0.0338	0.0136	1.26E-02	1
rs7684221	4	17957354	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0701	0.1902	1.85E-08	-1.1387	0.3676	1.96E-03	-0.0340	0.0136	1.23E-02	1
rs7686082	4	17957576	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0681	0.19	1.91E-08	-1.1384	0.3675	1.96E-03	-0.0338	0.0136	1.28E-02	1
rs7673321	4	17957688	3	17792249	18035250	A	T	0.1272	LCORL	intronic	-1.0557	0.1902	2.84E-08	-1.0771	0.3679	3.43E-03	-0.0335	0.0136	1.37E-02	1
rs7690823	4	17957698	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0673	0.19	1.94E-08	-1.1391	0.3676	1.95E-03	-0.0338	0.0136	1.28E-02	1
rs10446630	4	17958690	3	17792249	18035250	C	G	0.1272	LCORL	intronic	1.0692	0.19	1.82E-08	1.1402	0.3674	1.92E-03	0.0338	0.0136	1.28E-02	1
rs13151431	4	17959581	3	17792249	18035250	A	C	0.1272	LCORL	intronic	-1.0672	0.1899	1.92E-08	-1.1646	0.3667	1.50E-03	-0.0338	0.0136	1.27E-02	1
rs13105471	4	17959776	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0545	0.1894	2.60E-08	-1.1646	0.3667	1.50E-03	-0.0328	0.0135	1.51E-02	1
rs11945359	4	17960008	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0729	0.1899	1.61E-08	1.1646	0.3667	1.50E-03	0.0338	0.0136	1.27E-02	1
rs11930366	4	17960168	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0675	0.1899	1.90E-08	-1.1641	0.3667	1.51E-03	-0.0338	0.0136	1.27E-02	1
rs1876219	4	17961415	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0666	0.1899	1.96E-08	-1.1647	0.3667	1.50E-03	-0.0338	0.0136	1.27E-02	1
rs7670435	4	17962260	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0663	0.1899	1.97E-08	-1.1646	0.3667	1.50E-03	-0.0338	0.0136	1.27E-02	1
rs7695840	4	17962379	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0604	0.1899	2.36E-08	1.1626	0.3667	1.53E-03	0.0338	0.0136	1.27E-02	1
rs16896155	4	17962935	3	17792249	18035250	A	T	0.1272	LCORL	intronic	1.0660	0.1899	2.00E-08	1.1646	0.3667	1.50E-03	0.0338	0.0136	1.26E-02	1
rs7662221	4	17966468	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0667	0.1899	1.95E-08	-1.1650	0.3667	1.50E-03	-0.0338	0.0136	1.26E-02	1
rs7697634	4	17966746	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0650	0.1899	2.06E-08	1.1680	0.3667	1.45E-03	0.0341	0.0136	1.20E-02	1
rs16896164	4	17967094	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0863	0.1907	1.22E-08	1.1587	0.3669	1.60E-03	0.0341	0.0136	1.19E-02	1
rs34588175	4	17967114	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0807	0.1906	1.43E-08	-1.1280	0.3679	2.18E-03	-0.0341	0.0136	1.19E-02	1
rs11933767	4	17967896	3	17792249	18035250	C	G	0.1272	LCORL	intronic	-1.0571	0.19	2.64E-08	-1.1387	0.3676	1.96E-03	-0.0339	0.0136	1.25E-02	1
rs34025766	4	17968811	3	17792249	18035250	A	T	0.1272	LCORL	intronic	-1.0617	0.19	2.31E-08	-1.1385	0.3674	1.95E-03	-0.0339	0.0136	1.25E-02	1
rs6853216	4	17970655	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0482	0.19	3.45E-08	-1.1317	0.3673	2.07E-03	-0.0340	0.0136	1.21E-02	1
rs11933575	4	17971138	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0567	0.1901	2.72E-08	1.1404	0.3673	1.91E-03	0.0339	0.0136	1.25E-02	1
rs11930105	4	17972078	3	17792249	18035250	A	C	0.1272	LCORL	intronic	-1.0576	0.19	2.59E-08	-1.1307	0.3675	2.10E-03	-0.0339	0.0136	1.24E-02	1
rs7661129	4	17973171	3	17792249	18035250	C	G	0.1272	LCORL	intronic	-1.0605	0.19	2.40E-08	-1.1383	0.3673	1.95E-03	-0.0339	0.0136	1.25E-02	1
rs11938188	4	17973698	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0605	0.19	2.40E-08	1.1382	0.3673	1.95E-03	0.0339	0.0136	1.26E-02	1
rs16896182	4	17973899	3	17792249	18035250	C	G	0.1272	LCORL	intronic	1.0600	0.19	2.42E-08	1.1316	0.3673	2.07E-03	0.0339	0.0136	1.25E-02	1
rs13144742	4	17974181	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0585	0.19	2.53E-08	1.1317	0.3673	2.07E-03	0.0348	0.0136	1.04E-02	1
rs12500636	4	17974883	3	17792249	18035250	T	G	0.1272	LCORL	intronic	1.0615	0.19	2.30E-08	1.1636	0.3665	1.50E-03	0.0339	0.0136	1.26E-02	1
rs12511456	4	17975603	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0602	0.19	2.42E-08	-1.1382	0.3673	1.95E-03	-0.0338	0.0136	1.27E-02	1
rs12501035	4	17976326	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0586	0.19	2.52E-08	1.1626	0.3667	1.53E-03	0.0338	0.0136	1.27E-02	1
rs13127416	4	17976779	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0585	0.19	2.53E-08	1.1626	0.3667	1.53E-03	0.0338	0.0136	1.27E-02	1
rs13152352	4	17976846	3	17792249	18035250	A	C	0.1272	LCORL	intronic	-1.0563	0.1901	2.73E-08	-1.1631	0.3667	1.52E-03	-0.0335	0.0136	1.38E-02	1
rs6449350	4	17977535	3	17792249	18035250	A	C	0.1272	LCORL	intronic	1.0588	0.1899	2.49E-08	1.1637	0.3665	1.50E-03	0.0338	0.0136	1.28E-02	1
rs34156351	4	17983055	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0543	0.19	2.89E-08	-1.1373	0.3676	1.99E-03	-0.0336	0.0136	1.33E-02	1
rs6839954	4	17984129	3	17792249	18035250	T	G	0.1272	LCORL	intronic	1.0580	0.19	2.55E-08	1.1637	0.3665	1.51E-03	0.0336	0.0136	1.33E-02	1
rs6840334	4	17984277	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0580	0.19	2.55E-08	1.1637	0.3665	1.50E-03	0.0336	0.0136	1.34E-02	1
rs6835186	4	17984316	3	17792249	18035250	A	C	0.1272	LCORL	intronic	1.0579	0.19	2.56E-08	1.1637	0.3665	1.50E-03	0.0336	0.0136	1.34E-02	1
rs6810665	4	17984462	3	17792249	18035250	A	C	0.1272	LCORL	intronic	-1.0628	0.1899	2.19E-08	-1.1637	0.3665	1.51E-03	-0.0333	0.0136	1.44E-02	1
rs35338009	4	17984842	3	17792249	18035250	T	G	0.1272	LCORL	intronic	-1.0528	0.191	3.55E-08	-1.1392	0.3674	1.94E-03	-0.0330	0.0136	1.53E-02	1
rs35565383	4	17984874	3	17792249	18035250	C	G	0.1272	LCORL	intronic	1.0354	0.1899	4.98E-08	1.1383	0.3674	1.95E-03	0.0327	0.0136	1.61E-02	1
rs67113817	4	17985189	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0571	0.19	2.62E-08	1.1636	0.3665	1.51E-03	0.0336	0.0136	1.35E-02	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs35210497	4	17985374	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0571	0.19	2.62E-08	1.1634	0.3665	1.51E-03	0.0336	0.0136	1.35E-02	1
rs1987068	4	17986522	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0563	0.19	2.72E-08	-1.1382	0.3674	1.96E-03	-0.0336	0.0136	1.35E-02	1
rs35317957	4	17986863	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0563	0.19	2.72E-08	1.1382	0.3674	1.96E-03	0.0335	0.0136	1.36E-02	1
rs7668933	4	17988141	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0601	0.19	2.41E-08	1.1321	0.3673	2.06E-03	0.0331	0.0136	1.49E-02	1
rs35348660	4	17988635	3	17792249	18035250	A	T	0.1272	LCORL	intronic	-1.0571	0.19	2.65E-08	-1.1627	0.3667	1.53E-03	-0.0335	0.0136	1.38E-02	1
rs13132994	4	17990181	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0558	0.19	2.77E-08	1.1383	0.3674	1.95E-03	0.0335	0.0136	1.37E-02	1
rs67978911	4	17991423	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0568	0.19	2.65E-08	-1.1637	0.3665	1.50E-03	-0.0335	0.0136	1.38E-02	1
rs16896210	4	17992332	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0638	0.1919	2.95E-08	1.1564	0.3665	1.61E-03	0.0325	0.0139	1.91E-02	1
rs16896213	4	17994661	3	17792249	18035250	C	G	0.1272	LCORL	intronic	1.0577	0.1899	2.57E-08	1.1630	0.3664	1.51E-03	0.0336	0.0136	1.34E-02	1
rs34358941	4	17995047	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0580	0.19	2.55E-08	1.1632	0.3664	1.51E-03	0.0336	0.0136	1.34E-02	1
rs16896215	4	17995312	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0574	0.19	2.60E-08	1.1632	0.3664	1.51E-03	0.0336	0.0136	1.34E-02	1
rs6843651	4	17995500	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0574	0.19	2.60E-08	1.1633	0.3664	1.51E-03	0.0336	0.0136	1.34E-02	1
rs6824748	4	17997066	3	17792249	18035250	A	G	0.1272	LCORL	intronic	-1.0517	0.1901	3.15E-08	-1.1336	0.3673	2.04E-03	-0.0337	0.0136	1.32E-02	1
rs12513171	4	17997541	3	17792249	18035250	T	C	0.1292	LCORL	intronic	1.0489	0.19	3.36E-08	1.1338	0.3672	2.02E-03	0.0343	0.0136	1.17E-02	1
rs16896236	4	18003812	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0704	0.19	1.77E-08	1.1769	0.3664	1.33E-03	0.0337	0.0136	1.32E-02	1
rs6821168	4	18005019	3	17792249	18035250	A	C	0.1272	LCORL	intronic	1.0561	0.1901	2.78E-08	1.1488	0.3675	1.78E-03	0.0337	0.0136	1.32E-02	1
rs16896245	4	18005608	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0511	0.1902	3.25E-08	-1.1488	0.3675	1.78E-03	-0.0338	0.0136	1.30E-02	1
rs35613046	4	18005966	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0520	0.1901	3.16E-08	1.1487	0.3675	1.78E-03	0.0338	0.0136	1.30E-02	1
rs6828122	4	18006052	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0503	0.1902	3.32E-08	1.1487	0.3675	1.78E-03	0.0338	0.0136	1.31E-02	1
rs12513324	4	18006951	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0640	0.192	2.97E-08	-1.1388	0.3673	1.94E-03	-0.0335	0.0140	1.66E-02	1
rs2085683	4	18007435	3	17792249	18035250	C	G	0.1272	LCORL	intronic	1.0525	0.1902	3.11E-08	1.1367	0.3676	1.99E-03	0.0338	0.0136	1.30E-02	1
rs6842114	4	18008199	3	17792249	18035250	A	C	0.1272	LCORL	intronic	1.0564	0.1901	2.74E-08	1.1570	0.3667	1.61E-03	0.0339	0.0136	1.29E-02	1
rs6849629	4	18009488	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0551	0.1902	2.88E-08	1.1378	0.3673	1.96E-03	0.0339	0.0136	1.28E-02	1
rs6811842	4	18009798	3	17792249	18035250	A	T	0.1272	LCORL	intronic	-1.0584	0.19	2.56E-08	-1.1368	0.3676	1.99E-03	-0.0342	0.0136	1.21E-02	1
rs16896271	4	18012454	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0549	0.1901	2.88E-08	1.1368	0.3675	1.99E-03	0.0337	0.0137	1.38E-02	1
rs10516315	4	18016877	3	17792249	18035250	A	G	0.1272	LCORL	intronic	1.0595	0.19	2.47E-08	1.1627	0.3664	1.51E-03	0.0337	0.0137	1.38E-02	1
rs6830062	4	18017730	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0560	0.19	2.71E-08	1.1941	0.3660	1.11E-03	0.0338	0.0137	1.34E-02	1
rs35081654	4	18017938	3	17792249	18035250	A	T	0.1272	LCORL	intronic	1.0591	0.19	2.50E-08	1.1629	0.3664	1.51E-03	0.0336	0.0137	1.41E-02	1
rs6831102	4	18018236	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0585	0.1901	2.57E-08	1.1629	0.3664	1.51E-03	0.0336	0.0137	1.43E-02	1
rs1585334	4	18018944	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0602	0.1901	2.46E-08	-1.1630	0.3664	1.51E-03	-0.0337	0.0137	1.40E-02	1
rs1585333	4	18019025	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0602	0.1901	2.46E-08	1.1629	0.3664	1.51E-03	0.0335	0.0137	1.45E-02	1
rs7698271	4	18019413	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0604	0.1901	2.45E-08	-1.1629	0.3664	1.51E-03	-0.0335	0.0137	1.45E-02	1
rs7698644	4	18019572	3	17792249	18035250	T	C	0.1272	LCORL	intronic	-1.0672	0.1901	1.98E-08	-1.1629	0.3664	1.51E-03	-0.0335	0.0137	1.46E-02	1
rs7659195	4	18022692	3	17792249	18035250	T	C	0.1272	LCORL	intronic	1.0710	0.1956	4.36E-08	1.1629	0.3664	1.51E-03	0.0342	0.0144	1.73E-02	1
rs1380294	4	18024121	3	17792249	18035250	T	C	0.1272	LCORL	upstream	-1.0630	0.1904	2.35E-08	-1.1304	0.3673	2.09E-03	-0.0331	0.0138	1.62E-02	1
rs7668417	4	18025029	3	17792249	18035250	A	G	0.1272	LCORL	intergenic	-1.0636	0.1905	2.38E-08	-1.1449	0.3673	1.83E-03	-0.0331	0.0138	1.64E-02	1
rs2125654	4	18025368	3	17792249	18035250	A	T	0.1272	LCORL	intergenic	-1.0644	0.1906	2.34E-08	-1.1496	0.3668	1.73E-03	-0.0330	0.0138	1.66E-02	1
rs1380293	4	18027235	3	17792249	18035250	T	C	0.1272	LCORL	intergenic	1.0646	0.1906	2.33E-08	1.1674	0.3657	1.42E-03	0.0328	0.0138	1.74E-02	1
rs7694606	4	18028987	3	17792249	18035250	A	G	0.1272	LCORL	intergenic	-1.0548	0.1909	3.26E-08	-1.1585	0.3669	1.60E-03	-0.0330	0.0139	1.72E-02	1
rs7694806	4	18029100	3	17792249	18035250	A	G	0.1272	LCORL	intergenic	-1.0582	0.1909	2.97E-08	-1.1477	0.3669	1.77E-03	-0.0329	0.0139	1.76E-02	1
rs7696532	4	18029299	3	17792249	18035250	T	C	0.1272	LCORL	intergenic	-1.0595	0.1908	2.82E-08	-1.1429	0.3666	1.83E-03	-0.0327	0.0139	1.85E-02	1
rs16896312	4	18030853	3	17792249	18035250	T	C	0.1272	LCORL	intergenic	-1.0581	0.1912	3.11E-08	-1.1732	0.3660	1.36E-03	-0.0323	0.0139	2.06E-02	1
rs6449353	4	18033488	3	17792249	18035250	T	C	0.1272	LCORL	intergenic	1.0675	0.1919	2.67E-08	1.1658	0.3655	1.43E-03	0.0323	0.0141	2.20E-02	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs13107325	4	103188709	4	103001649	103387161	T	C	0.07952	SLC39A8	exonic	1.5264	0.279	4.47E-08	0.8030	0.5276	1.28E-01	0.0590	0.0208	4.62E-03	0
rs13109272	4	103292422	4	103001649	103387161	T	C	0.07654	SLC39A8	NA	-1.4937	0.2679	2.46E-08	-1.1935	0.5276	2.37E-02	-0.0546	0.0195	5.06E-03	1
rs2301718	4	106009763	5	106009763	106009763	A	G	0.2286	RP11-556I14.1	ncRNA_intronic	0.9752	0.1649	3.32E-09	0.2256	0.3311	4.96E-01	0.0451	0.0118	1.32E-04	0
rs2764264	6	108934461	6	108861264	109019323	T	C	0.3728	FOXO3	intronic	0.8178	0.1481	3.34E-08	1.2551	0.2906	1.60E-05	0.0408	0.0108	1.51E-04	1
rs2022464	6	108945370	6	108861264	109019323	A	C	0.3648	FOXO3	intronic	-0.8338	0.1483	1.88E-08	-1.1162	0.2923	1.36E-04	-0.0437	0.0108	5.21E-05	1
rs10457180	6	108965039	6	108861264	109019323	A	G	0.3678	FOXO3	intronic	0.8338	0.1482	1.84E-08	1.1101	0.2921	1.46E-04	0.0433	0.0108	5.94E-05	1
rs13217795	6	108974098	6	108861264	109019323	T	C	0.3658	FOXO3	intronic	0.8365	0.1484	1.73E-08	1.0821	0.2931	2.24E-04	0.0430	0.0108	6.63E-05	1
rs4946932	6	108974746	6	108861264	109019323	A	C	0.3668	FOXO3	intronic	-0.8408	0.1482	1.41E-08	-1.0950	0.2924	1.83E-04	-0.0437	0.0108	5.00E-05	1
rs9400239	6	108977663	6	108861264	109019323	T	C	0.3678	FOXO3	UTR5	-0.8456	0.1482	1.17E-08	-1.0976	0.2925	1.76E-04	-0.0439	0.0108	4.54E-05	1
rs2153960	6	108988184	6	108861264	109019323	A	G	0.3579	FOXO3	intronic	0.8127	0.1486	4.54E-08	0.8810	0.2944	2.77E-03	0.0434	0.0108	5.58E-05	1
rs35396874	6	108994433	6	108861264	109019323	T	C	0.3519	FOXO3	intronic	0.8352	0.1495	2.34E-08	0.8850	0.2959	2.79E-03	0.0421	0.0108	9.87E-05	1
rs9398172	6	108994826	6	108861264	109019323	A	G	0.3519	FOXO3	intronic	0.8303	0.1496	2.86E-08	0.8682	0.2963	3.40E-03	0.0421	0.0108	9.68E-05	1
rs61192764	6	108995187	6	108861264	109019323	A	G	0.1581	FOXO3	intronic	1.1803	0.2082	1.44E-08	1.0491	0.4085	1.02E-02	0.0432	0.0150	3.99E-03	1
rs3800228	6	108996748	6	108861264	109019323	T	G	0.3469	FOXO3	intronic	-0.8269	0.15	3.53E-08	-0.8599	0.2974	3.85E-03	-0.0424	0.0108	9.24E-05	1
rs3800229	6	108996963	6	108861264	109019323	T	G	0.3499	FOXO3	intronic	0.8255	0.1496	3.45E-08	0.8666	0.2966	3.50E-03	0.0427	0.0108	7.66E-05	1
rs9374040	6	108997435	6	108861264	109019323	A	G	0.3499	FOXO3	intronic	0.8241	0.1497	3.69E-08	0.8664	0.2967	3.51E-03	0.0428	0.0108	7.46E-05	1
rs9400240	6	108997611	6	108861264	109019323	A	G	0.3499	FOXO3	intronic	0.8232	0.1497	3.78E-08	0.8671	0.2967	3.49E-03	0.0428	0.0108	7.56E-05	1
rs3800230	6	108998128	6	108861264	109019323	T	G	0.1581	FOXO3	intronic	1.1733	0.2084	1.79E-08	1.0466	0.4091	1.05E-02	0.0433	0.0150	3.93E-03	1
rs1935952	6	108998905	6	108861264	109019323	C	G	0.3509	FOXO3	intronic	0.8331	0.1497	2.62E-08	0.8859	0.2967	2.84E-03	0.0430	0.0108	6.96E-05	1
rs3800232	6	108998953	6	108861264	109019323	T	C	0.1581	FOXO3	intronic	-1.1713	0.2084	1.90E-08	-1.0413	0.4092	1.10E-02	-0.0434	0.0150	3.85E-03	1
rs1935951	6	108999101	6	108861264	109019323	A	G	0.3499	FOXO3	intronic	0.8255	0.1497	3.51E-08	0.8677	0.2970	3.50E-03	0.0429	0.0108	7.23E-05	1
rs1935949	6	108999287	6	108861264	109019323	A	G	0.3499	FOXO3	intronic	-0.8263	0.1497	3.40E-08	-0.8669	0.2970	3.53E-03	-0.0429	0.0108	7.26E-05	1
rs9398173	6	109000316	6	108861264	109019323	T	C	0.3489	FOXO3	intronic	-0.8641	0.1558	2.94E-08	-0.8602	0.2973	3.83E-03	-0.0395	0.0113	4.64E-04	1
rs4946935	6	109000742	6	108861264	109019323	A	G	0.3479	FOXO3	intronic	-0.8255	0.1502	3.86E-08	-0.8943	0.2981	2.71E-03	-0.0429	0.0109	7.87E-05	1
rs4945816	6	109002042	6	108861264	109019323	T	C	0.3499	FOXO3	UTR3	0.8469	0.1504	1.79E-08	0.8703	0.2976	3.46E-03	0.0441	0.0109	5.28E-05	1
rs4946936	6	109003321	6	108861264	109019323	T	C	0.3499	FOXO3	UTR3	-0.8455	0.1503	1.87E-08	-0.8754	0.2978	3.29E-03	-0.0436	0.0109	6.17E-05	1
rs9388490	6	126704795	7	126648460	127369230	T	C	0.4414	CENPW	intergenic	0.8320	0.1386	1.95E-09	1.5643	0.2707	7.94E-09	0.0545	0.0100	5.76E-08	1
rs11759026	6	126792095	7	126648460	127369230	A	G	0.2545	MIR588	intergenic	-1.5906	0.1729	3.58E-20	-1.5237	0.3193	1.87E-06	-0.0811	0.0123	4.51E-11	1
rs1490384	6	126851160	7	126648460	127369230	T	C	0.493	MIR588	intergenic	0.7445	0.1365	4.91E-08	1.5604	0.2669	5.25E-09	0.0494	0.0099	5.94E-07	1
rs4273712	6	126964510	7	126648460	127369230	A	G	0.2803	PRELID1P1	upstream	-1.3614	0.157	4.34E-18	-1.3746	0.3017	5.29E-06	-0.0807	0.0113	1.12E-12	1
rs1262474	6	126976071	7	126648460	127369230	C	G	0.2416	PRELID1P1	intergenic	0.9648	0.1586	1.19E-09	1.2168	0.3060	7.06E-05	0.0453	0.0116	9.22E-05	1
rs1262476	6	126986996	7	126648460	127369230	A	G	0.2406	RPS4XP9	intergenic	-0.9717	0.1582	8.10E-10	-1.2103	0.3060	7.72E-05	-0.0457	0.0116	7.90E-05	1
rs13212044	6	127025661	7	126648460	127369230	T	G	0.2416	RPS4XP9	intergenic	-0.9598	0.1581	1.28E-09	-1.2103	0.3056	7.55E-05	-0.0470	0.0116	4.95E-05	1
rs10484759	6	127037042	7	126648460	127369230	T	C	0.2316	RPS4XP9	intergenic	-0.9684	0.1601	1.46E-09	-1.2024	0.3106	1.09E-04	-0.0477	0.0117	4.73E-05	1
rs853974	6	127068983	7	126648460	127369230	T	C	0.2753	RPS4XP9	intergenic	1.3524	0.1576	9.28E-18	1.4284	0.3043	2.74E-06	0.0775	0.0115	1.83E-11	1
rs12525327	6	127107248	7	126648460	127369230	A	G	0.2435	RPS4XP9	intergenic	0.9502	0.1625	4.95E-09	1.1350	0.3049	1.99E-04	0.0488	0.0122	6.74E-05	1
rs35848181	6	127118646	7	126648460	127369230	A	G	0.2396	RPS4XP9	intergenic	-0.9572	0.162	3.46E-09	-1.0865	0.3031	3.40E-04	-0.0496	0.0122	4.93E-05	1
rs9375477	6	127204623	7	126648460	127369230	A	G	0.163	RPS4XP9	intergenic	-1.2224	0.191	1.57E-10	-0.7766	0.3722	3.70E-02	-0.0687	0.0141	1.13E-06	1
rs139849708	6	127369230	7	126648460	127369230	T	C	0.02087	RSPO3	intergenic	2.7827	0.4746	4.53E-09	0.3436	0.8553	6.88E-01	NA	NA	NA	NA
rs149352678	7	54920906	8	54909928	55015505	T	C	0.1203	SNORA73	intergenic	1.3946	0.2439	1.08E-08	2.1007	0.4663	6.75E-06	0.0399	0.0173	2.08E-02	1
rs76928645	7	54941328	8	54909928	55015505	T	C	0.1272	SNORA73	intergenic	1.3466	0.2352	1.04E-08	2.0573	0.4440	3.66E-06	0.0355	0.0168	3.41E-02	1
rs151057105	7	54944920	8	54909928	55015505	T	C	0.1213	SNORA73	intergenic	1.4185	0.2442	6.32E-09	2.1533	0.4619	3.20E-06	0.0347	0.0172	4.37E-02	1
rs74504435	7	54949256	8	54909928	55015505	A	G	0.1213	SNORA73	intergenic	-1.3984	0.2457	1.26E-08	-2.1608	0.4665	3.70E-06	-0.0375	0.0173	3.04E-02	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs77126132	7	54966738	8	54909928	55015505	A	G	0.1203	SNORA73	intergenic	1.4570	0.2472	3.78E-09	2.2156	0.4656	2.00E-06	0.0398	0.0176	2.39E-02	1
rs77324770	7	155772027	9	155772027	155778152	T	C	0.05964	AC021218.2	intergenic	-1.9547	0.3499	2.32E-08	-1.2594	0.5246	1.64E-02	NA	NA	NA	NA
rs75745313	7	155778152	9	155772027	155778152	A	G	0.05964	AC021218.2	intergenic	-1.9833	0.3522	1.80E-08	-1.1903	0.5218	2.26E-02	NA	NA	NA	NA
rs10883848	10	104973061	10	104591182	105175131	A	G	0.34	ST13P13	intergenic	0.8478	0.1505	1.76E-08	0.5639	0.2863	4.89E-02	0.0575	0.0109	1.53E-07	1
rs6584545	10	104999266	10	104591182	105175131	A	T	0.2525	RPEL1	intergenic	0.9854	0.1663	3.13E-09	0.5240	0.3136	9.48E-02	0.0710	0.0119	2.74E-09	0
rs1628768	10	105012994	10	104591182	105175131	T	C	0.2555	RPEL1	intergenic	-0.9972	0.1662	1.99E-09	-0.5130	0.3136	1.02E-01	-0.0723	0.0119	1.24E-09	0
rs2487862	10	105045477	10	104591182	105175131	T	C	0.2535	INA	intronic	1.0330	0.1746	3.32E-09	0.5131	0.3146	1.03E-01	0.0758	0.0131	7.48E-09	0
rs2030205	10	105056473	10	104591182	105175131	C	G	0.2545	PCGF6	intergenic	0.9600	0.1667	8.51E-09	0.5014	0.3147	1.11E-01	0.0729	0.0120	1.38E-09	0
rs4420190	10	105085191	10	104591182	105175131	T	C	0.2555	PCGF6	intronic	-0.9257	0.1665	2.71E-08	-0.5476	0.3153	8.24E-02	-0.0712	0.0120	3.30E-09	0
rs72846192	10	105091459	10	104591182	105175131	A	C	0.2545	PCGF6	intronic	-0.9323	0.1671	2.41E-08	-0.5292	0.3153	9.34E-02	-0.0721	0.0121	2.40E-09	0
rs4311992	10	105120649	10	104591182	105175131	A	G	0.2505	TAF5	intergenic	0.9480	0.1674	1.48E-08	0.4899	0.3158	1.21E-01	0.0723	0.0122	2.94E-09	0
rs55948574	11	17310391	11	17067849	17365209	T	C	0.2793	NUCB2	intronic	0.8248	0.1502	3.96E-08	0.0138	0.2944	9.63E-01	0.0031	0.0109	7.77E-01	0
rs3911562	11	92355990	12	92317858	92558342	A	T	0.336	FAT3	intronic	0.7941	0.1455	4.83E-08	0.3092	0.2900	2.86E-01	0.0325	0.0103	1.69E-03	0
rs1791558	11	92356881	12	92317858	92558342	A	G	0.339	FAT3	intronic	-0.7920	0.1452	4.94E-08	-0.3188	0.2897	2.71E-01	-0.0323	0.0103	1.76E-03	0
rs1613721	11	92357002	12	92317858	92558342	A	G	0.339	FAT3	intronic	-0.7924	0.1452	4.85E-08	-0.3232	0.2897	2.65E-01	-0.0323	0.0103	1.76E-03	0
rs56021037	11	92363215	12	92317858	92558342	T	C	0.336	FAT3	intronic	-0.7935	0.1455	4.89E-08	-0.3066	0.2896	2.90E-01	-0.0314	0.0104	2.41E-03	0
rs10830949	11	92540758	12	92317858	92558342	T	C	0.328	FAT3	intronic	-0.8014	0.1469	4.93E-08	-0.2978	0.2919	3.08E-01	-0.0352	0.0104	7.24E-04	0
rs12298541	12	66306441	13	66257355	66389968	A	C	0.341	HMGA2:AC090673	intronic	0.8290	0.1477	2.00E-08	0.7320	0.2826	9.61E-03	0.0612	0.0110	2.31E-08	1
rs343086	12	66325689	13	66257355	66389968	T	C	0.3032	HMGA2	intronic	-0.8945	0.1501	2.53E-09	-0.7404	0.2908	1.09E-02	-0.0533	0.0110	1.25E-06	1
rs1480474	12	66326943	13	66257355	66389968	A	G	0.4563	HMGA2	intronic	0.9000	0.1397	1.19E-10	1.1525	0.2698	1.97E-05	0.0555	0.0100	3.07E-08	1
rs10878349	12	66327632	13	66257355	66389968	A	G	0.4563	HMGA2	intronic	1.0999	0.1385	2.01E-15	1.3509	0.2701	5.88E-07	0.0585	0.0099	3.50E-09	1
rs1038196	12	66343400	13	66257355	66389968	C	G	0.4573	HMGA2	intronic	-1.0574	0.1371	1.26E-14	-1.3437	0.2693	6.20E-07	NA	NA	NA	NA
rs10784502	12	66343810	13	66257355	66389968	T	C	0.4583	HMGA2	intronic	-1.0612	0.1372	1.02E-14	-1.3513	0.2693	5.36E-07	-0.0571	0.0098	5.67E-09	1
rs1979440	12	66346624	13	66257355	66389968	T	C	0.4433	HMGA2	UTR3	0.8671	0.1402	6.20E-10	1.0719	0.2701	7.31E-05	0.0504	0.0101	5.69E-07	1
rs7959830	12	66347368	13	66257355	66389968	T	G	0.4513	HMGA2	UTR3	-0.8618	0.1391	5.80E-10	-1.1403	0.2696	2.38E-05	-0.0534	0.0100	9.62E-08	1
rs1351394	12	66351826	13	66257355	66389968	T	C	0.4503	HMGA2	UTR3	1.0888	0.1384	3.63E-15	1.3310	0.2695	8.04E-07	0.0570	0.0098	6.54E-09	1
rs7138102	12	66353891	13	66257355	66389968	A	G	0.4354	HMGA2	intronic	-0.7934	0.1405	1.61E-08	-0.9293	0.2722	6.44E-04	-0.0499	0.0102	9.19E-07	1
rs867633	12	66354911	13	66257355	66389968	A	G	0.4354	HMGA2	intronic	-0.8061	0.1406	9.93E-09	-0.9463	0.2722	5.11E-04	-0.0505	0.0102	6.53E-07	1
rs1042725	12	66358347	13	66257355	66389968	T	C	0.4632	HMGA2	UTR3	-1.0669	0.1376	8.94E-15	-1.2216	0.2694	5.89E-06	-0.0560	0.0098	1.21E-08	1
rs8756	12	66359752	13	66257355	66389968	A	C	0.4473	HMGA2	UTR3	-1.0735	0.1373	5.30E-15	-1.5180	0.2694	1.83E-08	-0.0557	0.0098	1.26E-08	1
rs7970350	12	66360164	13	66257355	66389968	T	C	0.4632	HMGA2	downstream	-1.0625	0.1375	1.11E-14	-1.2226	0.2695	5.82E-06	-0.0553	0.0098	1.75E-08	1
rs7968902	12	66363070	13	66257355	66389968	T	G	0.4076	HMGA2	intergenic	0.9456	0.1397	1.30E-11	1.1022	0.2753	6.32E-05	0.0547	0.0102	7.93E-08	1
rs61921611	12	66367726	13	66257355	66389968	T	C	0.338	HMGA2	intergenic	0.9190	0.1482	5.67E-10	1.0801	0.2936	2.37E-04	0.0412	0.0107	1.10E-04	1
rs7968682	12	66371880	13	66257355	66389968	T	G	0.4473	HMGA2	intergenic	-1.0756	0.1379	6.32E-15	-1.5048	0.2703	2.70E-08	-0.0559	0.0099	1.49E-08	1
NA	12	66373602	13	66257355	66389968	T	C	0.4473	HMGA2	intergenic	-1.1921	0.2052	6.30E-09	-1.4941	0.2709	3.60E-08	-0.0560	0.0103	5.24E-08	1
NA	12	66374247	13	66257355	66389968	A	G	0.4473	HMGA2	intergenic	1.3211	0.2382	2.93E-08	1.5142	0.2711	2.42E-08	0.0693	0.0115	1.88E-09	1
rs9669278	12	66374587	13	66257355	66389968	T	C	0.4473	HMGA2	intergenic	1.1151	0.1403	1.86E-15	1.4970	0.2708	3.38E-08	0.0572	0.0101	1.30E-08	1
rs7306710	12	66376091	13	66257355	66389968	T	C	0.4463	HMGA2	intergenic	1.1329	0.1405	7.56E-16	1.5214	0.2708	2.01E-08	0.0573	0.0101	1.48E-08	1
NA	12	66376202	13	66257355	66389968	C	G	0.4463	HMGA2	intergenic	-1.1938	0.2033	4.32E-09	-1.5255	0.2717	2.06E-08	NA	NA	NA	NA
rs1585897	12	66383320	13	66257355	66389968	A	C	0.4215	HMGA2	intergenic	-1.0364	0.1405	1.60E-13	-1.2410	0.2714	4.92E-06	-0.0471	0.0101	2.85E-06	1
rs7966895	12	66383843	13	66257355	66389968	A	G	0.338	HMGA2	intergenic	0.9027	0.1472	8.54E-10	1.4106	0.2844	7.23E-07	0.0338	0.0105	1.27E-03	1
rs11175990	12	66386396	13	66257355	66389968	T	C	0.2475	HMGA2	intergenic	0.9150	0.1668	4.15E-08	1.3119	0.3162	3.38E-05	0.0409	0.0121	7.39E-04	1
rs10748027	12	66387621	13	66257355	66389968	A	T	0.2952	HMGA2	intergenic	0.8781	0.1606	4.57E-08	0.8900	0.2980	2.83E-03	0.0491	0.0127	1.08E-04	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs10400419	12	66389968	13	66257355	66389968	T	C	0.4324	HMGA2	intergenic	0.9381	0.14	2.09E-11	1.3632	0.2760	8.06E-07	0.0455	0.0101	6.38E-06	1
rs35227403	12	68216239	14	68216239	68225876	A	T	0.05368	RP11-43N5.1	intergenic	-1.7779	0.3182	2.31E-08	-2.2433	0.5797	1.10E-04	-0.0760	0.0239	1.45E-03	1
rs28792763	15	90081905	15	90081905	90208310	A	G	0.4632	RP11-429B14.1	ncRNA_intronic	0.8393	0.1489	1.72E-08	0.4019	0.2773	1.47E-01	0.0139	0.0110	2.08E-01	0
rs1596062	15	90091513	15	90081905	90208310	A	C	0.4652	RP11-429B14.1	ncRNA_intronic	0.8061	0.1471	4.23E-08	0.3038	0.2729	2.66E-01	0.0120	0.0108	2.68E-01	0
rs11630039	15	90123991	15	90081905	90208310	T	C	0.4831	RP11-429B14.1:TI	ncRNA_intronic	0.8263	0.1383	2.30E-09	0.3007	0.2710	2.67E-01	0.0085	0.0099	3.93E-01	0
rs893725	15	90128223	15	90081905	90208310	A	C	0.3777	RP11-429B14.1:TI	ncRNA_intronic	0.9023	0.14	1.15E-10	0.5440	0.2743	4.74E-02	0.0116	0.0101	2.51E-01	0
rs11639246	15	90128834	15	90081905	90208310	A	G	0.4851	RP11-429B14.1:TI	ncRNA_intronic	0.8145	0.1375	3.19E-09	0.3128	0.2708	2.48E-01	0.0080	0.0099	4.18E-01	0
rs11629584	15	90128966	15	90081905	90208310	T	C	0.4871	RP11-429B14.1:TI	exonic	0.7978	0.1375	6.53E-09	0.3234	0.2705	2.32E-01	0.0075	0.0099	4.46E-01	0
rs4932136	15	90132578	15	90081905	90208310	C	G	0.4831	RP11-429B14.1:TI	ncRNA_intronic	-0.8462	0.1393	1.24E-09	-0.3500	0.2705	1.96E-01	NA	NA	NA	NA
rs35892197	15	90135172	15	90081905	90208310	T	C	0.4821	RP11-429B14.1:TI	ncRNA_exonic	0.8324	0.1377	1.48E-09	0.3459	0.2704	2.01E-01	0.0085	0.0098	3.91E-01	0
rs8032553	15	90137325	15	90081905	90208310	A	G	0.4831	TICRR	intronic	-0.8395	0.1377	1.08E-09	-0.3343	0.2708	2.17E-01	-0.0084	0.0098	3.92E-01	0
rs4556765	15	90139262	15	90081905	90208310	T	C	0.4821	TICRR	intronic	0.8317	0.1376	1.51E-09	0.3266	0.2704	2.27E-01	0.0076	0.0098	4.39E-01	0
rs11634571	15	90195712	15	90081905	90208310	A	G	0.4881	KIF7	intronic	0.8506	0.1415	1.85E-09	0.2488	0.2704	3.58E-01	0.0102	0.0102	3.18E-01	0
rs11652522	17	43055579	16	43055579	43055579	A	C	0.0835	CTD-2534I21.9	intergenic	-1.2996	0.2299	1.59E-08	-0.5817	0.4502	1.96E-01	-0.0438	0.0165	7.74E-03	0
rs117642368	17	43399058	17	43399058	44874453	C	G	0.1014	MAP3K14	intergenic	-1.6616	0.2435	8.94E-12	-1.6470	0.4427	2.01E-04	-0.0634	0.0203	1.73E-03	1
rs17686238	17	43417273	17	43399058	44874453	T	G	0.1054	RNA5SP443	intergenic	-1.9576	0.328	2.39E-09	-1.5384	0.4397	4.70E-04	-0.0577	0.0216	7.64E-03	1
rs62064594	17	43460181	17	43399058	44874453	A	G	0.1581	CTB-39G8.2	intergenic	-2.1586	0.2826	2.21E-14	-1.6112	0.3883	3.39E-05	-0.0933	0.0210	8.57E-06	1
rs62064595	17	43460374	17	43399058	44874453	A	G	0.16	ARHGAP27	intergenic	2.1324	0.2823	4.21E-14	1.6341	0.3859	2.33E-05	0.0923	0.0209	1.05E-05	1
rs61572747	17	43460891	17	43399058	44874453	A	G	0.2893	ARHGAP27	intergenic	1.7478	0.2293	2.48E-14	1.0532	0.3114	7.23E-04	NA	NA	NA	NA
rs79724577	17	43463493	17	43399058	44874453	A	C	0.1918	ARHGAP27	intergenic	2.1791	0.2466	1.00E-18	1.9384	0.3514	3.59E-08	0.1150	0.0157	2.02E-13	1
rs4763	17	43471489	17	43399058	44874453	A	G	0.1909	ARHGAP27	UTR3	-2.1628	0.2471	2.09E-18	-1.9442	0.3500	2.89E-08	-0.1184	0.0157	4.49E-14	1
rs62064597	17	43473307	17	43399058	44874453	C	G	0.1909	ARHGAP27	intronic	2.1355	0.2471	5.47E-18	2.0340	0.3503	6.70E-09	0.1183	0.0156	3.44E-14	1
rs62064598	17	43474668	17	43399058	44874453	C	G	0.1938	ARHGAP27:CTB-39	ncRNA_intronic	2.1222	0.2441	3.51E-18	1.9805	0.3504	1.65E-08	0.1178	0.0152	7.82E-15	1
rs2028078	17	43475929	17	43399058	44874453	A	G	0.1938	ARHGAP27	intronic	-2.1143	0.2444	5.15E-18	-1.9825	0.3503	1.59E-08	-0.1178	0.0152	7.59E-15	1
rs56220387	17	43476807	17	43399058	44874453	A	G	0.1918	ARHGAP27	intronic	2.1123	0.2443	5.24E-18	2.0181	0.3509	9.30E-09	0.1176	0.0151	8.29E-15	1
rs55793500	17	43479748	17	43399058	44874453	T	C	0.1938	ARHGAP27	intronic	2.1184	0.244	3.91E-18	1.9971	0.3498	1.19E-08	0.1179	0.0151	6.72E-15	1
rs62064600	17	43480701	17	43399058	44874453	A	G	0.1938	ARHGAP27	intronic	-2.1165	0.2439	3.98E-18	-1.9977	0.3498	1.18E-08	-0.1181	0.0151	6.03E-15	1
rs56236914	17	43483551	17	43399058	44874453	T	C	0.1938	ARHGAP27	intronic	-2.1355	0.2437	1.89E-18	-1.9967	0.3499	1.21E-08	-0.1182	0.0151	4.61E-15	1
rs62064603	17	43484496	17	43399058	44874453	T	C	0.1938	ARHGAP27	intronic	-2.1048	0.2431	4.81E-18	-1.9983	0.3499	1.17E-08	-0.1183	0.0151	4.19E-15	1
rs73984391	17	43484598	17	43399058	44874453	T	G	0.1938	ARHGAP27	intronic	-2.1458	0.2453	2.17E-18	-2.0051	0.3496	1.02E-08	-0.1177	0.0151	5.89E-15	1
NA	17	43484903	17	43399058	44874453	T	C	0.1938	ARHGAP27	intronic	2.3006	0.3023	2.71E-14	2.0937	0.3564	4.45E-09	0.1223	0.0161	3.11E-14	1
rs62064637	17	43485551	17	43399058	44874453	T	G	0.1938	ARHGAP27	intronic	2.1308	0.2435	2.10E-18	2.0054	0.3498	1.03E-08	0.1182	0.0151	4.13E-15	1
rs36078910	17	43487217	17	43399058	44874453	A	G	0.1968	ARHGAP27	intronic	-2.1047	0.2419	3.25E-18	-2.0332	0.3495	6.28E-09	-0.1177	0.0150	4.30E-15	1
rs35389313	17	43487424	17	43399058	44874453	T	C	0.1968	ARHGAP27	intronic	2.1133	0.2419	2.37E-18	2.0346	0.3495	6.13E-09	0.1182	0.0150	3.29E-15	1
rs35327136	17	43487574	17	43399058	44874453	A	C	0.1928	ARHGAP27	intronic	-2.1170	0.2433	3.27E-18	-2.0809	0.3499	2.89E-09	-0.1170	0.0150	5.58E-15	1
rs8071011	17	43488382	17	43399058	44874453	T	C	0.1968	ARHGAP27	intronic	-2.1077	0.2418	2.89E-18	-2.0378	0.3495	5.81E-09	-0.1176	0.0150	3.95E-15	1
rs62064641	17	43488792	17	43399058	44874453	T	C	0.1968	ARHGAP27	intronic	2.1109	0.2417	2.48E-18	2.0301	0.3492	6.42E-09	0.1176	0.0150	3.72E-15	1
rs62064643	17	43490853	17	43399058	44874453	A	G	0.1948	ARHGAP27	intronic	-2.1067	0.2428	4.04E-18	-2.0747	0.3500	3.25E-09	-0.1172	0.0149	3.56E-15	1
rs34063617	17	43491003	17	43399058	44874453	A	G	0.1968	ARHGAP27	intronic	-2.1129	0.2416	2.26E-18	-2.0406	0.3493	5.43E-09	-0.1177	0.0149	2.61E-15	1
rs12940792	17	43492357	17	43399058	44874453	T	C	0.1968	ARHGAP27	intronic	-2.1048	0.2414	2.76E-18	-2.0422	0.3493	5.27E-09	-0.1175	0.0149	2.51E-15	1
rs12947718	17	43493101	17	43399058	44874453	A	G	0.1968	ARHGAP27	intronic	-2.0986	0.2411	3.24E-18	-2.0426	0.3493	5.21E-09	-0.1177	0.0148	2.11E-15	1
rs71373560	17	43493504	17	43399058	44874453	T	C	0.1968	ARHGAP27	intronic	-2.1306	0.2435	2.15E-18	-2.0429	0.3492	5.18E-09	-0.1202	0.0152	2.28E-15	1
rs34915103	17	43493560	17	43399058	44874453	C	G	0.1968	ARHGAP27	intronic	2.1045	0.2413	2.77E-18	2.0430	0.3492	5.17E-09	0.1179	0.0148	1.58E-15	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs12942951	17	43493835	17	43399058	44874453	T	C	0.1909	ARHGAP27	intronic	2.1351	0.2472	5.76E-18	2.0433	0.3492	5.14E-09	0.1199	0.0157	2.09E-14	1
rs35884427	17	43495216	17	43399058	44874453	A	G	0.1968	ARHGAP27	intronic	-2.1042	0.2413	2.79E-18	-2.0430	0.3492	5.14E-09	-0.1179	0.0148	1.48E-15	1
NA	17	43495235	17	43399058	44874453	C	G	0.1968	ARHGAP27	intronic	2.1056	0.2749	1.88E-14	2.0843	0.3509	3.00E-09	0.1178	0.0148	1.50E-15	1
NA	17	43495420	17	43399058	44874453	A	T	0.1948	ARHGAP27	intronic	2.1992	0.313	2.13E-12	2.2590	0.3874	5.76E-09	0.1100	0.0188	5.12E-09	1
rs34286926	17	43495852	17	43399058	44874453	A	G	0.1958	ARHGAP27	intronic	2.0711	0.2376	2.90E-18	2.0733	0.3491	3.01E-09	0.1157	0.0145	1.51E-15	1
rs56378631	17	43496465	17	43399058	44874453	T	C	0.1958	ARHGAP27	intronic	2.0777	0.2377	2.29E-18	2.0745	0.3490	2.93E-09	0.1154	0.0145	1.52E-15	1
rs12946723	17	43496828	17	43399058	44874453	T	C	0.1958	ARHGAP27	intronic	-2.0839	0.2392	2.99E-18	-2.0748	0.3490	2.91E-09	-0.1163	0.0146	1.35E-15	1
rs12952764	17	43497210	17	43399058	44874453	A	G	0.1958	ARHGAP27	intronic	-2.0778	0.2378	2.40E-18	-2.0752	0.3490	2.89E-09	-0.1151	0.0144	1.61E-15	1
rs35420583	17	43498180	17	43399058	44874453	T	C	0.1958	ARHGAP27	intronic	-2.1433	0.2573	7.97E-17	-2.0759	0.3489	2.84E-09	-0.1250	0.0163	1.54E-14	1
rs34792542	17	43498181	17	43399058	44874453	A	G	0.1958	ARHGAP27	intronic	2.1573	0.2571	4.76E-17	2.0893	0.3507	2.71E-09	0.1249	0.0163	1.54E-14	1
rs35519908	17	43499328	17	43399058	44874453	T	C	0.1958	ARHGAP27	intronic	2.0736	0.2374	2.48E-18	2.0736	0.3489	2.95E-09	0.1148	0.0144	1.54E-15	1
rs12942666	17	43499839	17	43399058	44874453	A	G	0.1958	ARHGAP27	intronic	2.0736	0.2374	2.45E-18	2.0773	0.3488	2.74E-09	0.1148	0.0144	1.52E-15	1
rs62064645	17	43500477	17	43399058	44874453	A	G	0.1938	ARHGAP27	intronic	-2.0678	0.2388	4.82E-18	-2.1035	0.3495	1.86E-09	-0.1139	0.0143	2.00E-15	1
rs62064646	17	43500587	17	43399058	44874453	A	G	0.1958	ARHGAP27	intronic	-2.0900	0.239	2.22E-18	-2.0806	0.3485	2.51E-09	-0.1142	0.0143	1.68E-15	1
rs62064647	17	43500621	17	43399058	44874453	A	G	0.1958	ARHGAP27	intronic	-2.0720	0.2377	2.82E-18	-2.0775	0.3488	2.73E-09	-0.1145	0.0143	1.35E-15	1
rs7222389	17	43501442	17	43399058	44874453	T	C	0.1958	ARHGAP27	intronic	2.0669	0.237	2.73E-18	2.0903	0.3487	2.16E-09	0.1143	0.0143	1.38E-15	1
rs55648326	17	43501591	17	43399058	44874453	T	C	0.1958	ARHGAP27	intronic	2.0807	0.2383	2.53E-18	2.0933	0.3485	1.99E-09	0.1139	0.0143	1.73E-15	1
rs56212100	17	43501940	17	43399058	44874453	A	G	0.1968	ARHGAP27	intronic	-2.0672	0.237	2.75E-18	-2.0902	0.3487	2.16E-09	-0.1143	0.0143	1.39E-15	1
NA	17	43502012	17	43399058	44874453	T	C	0.214	ARHGAP27	intronic	2.1308	0.2734	6.57E-15	NA	NA	NA	0.1160	0.0145	1.30E-15	NA
rs62064649	17	43502111	17	43399058	44874453	A	G	0.1958	ARHGAP27	intronic	2.0867	0.2371	1.37E-18	2.0883	0.3487	2.24E-09	0.1141	0.0143	1.53E-15	1
rs35626715	17	43502241	17	43399058	44874453	T	C	0.1958	ARHGAP27	intronic	2.0831	0.2376	1.82E-18	2.0868	0.3487	2.30E-09	0.1145	0.0144	1.54E-15	1
rs62064651	17	43503000	17	43399058	44874453	A	G	0.1938	ARHGAP27	intronic	-2.0600	0.2382	5.21E-18	-2.1008	0.3494	1.94E-09	-0.1138	0.0143	1.66E-15	1
rs76344126	17	43503284	17	43399058	44874453	A	G	0.1938	ARHGAP27	intronic	-2.0662	0.2389	5.27E-18	-2.0978	0.3500	2.16E-09	-0.1137	0.0143	1.67E-15	1
rs7209501	17	43503294	17	43399058	44874453	A	C	0.1948	ARHGAP27	intronic	2.0637	0.2372	3.32E-18	2.0797	0.3491	2.71E-09	0.1139	0.0143	1.49E-15	1
rs12949256	17	43507297	17	43399058	44874453	T	C	0.1938	ARHGAP27	exonic	-2.1569	0.2441	9.79E-19	-2.1130	0.3492	1.53E-09	-0.1133	0.0145	6.31E-15	1
rs7220206	17	43507403	17	43399058	44874453	A	G	0.1938	ARHGAP27	exonic	-1.9788	0.2367	6.32E-17	-2.1205	0.3493	1.34E-09	-0.1127	0.0142	2.41E-15	1
rs7222444	17	43507649	17	43399058	44874453	A	G	0.1938	ARHGAP27	UTR5	2.0795	0.2392	3.52E-18	2.1140	0.3492	1.50E-09	0.1148	0.0143	1.21E-15	1
rs12939187	17	43508223	17	43399058	44874453	T	G	0.1938	ARHGAP27	intronic	-2.0472	0.2367	5.19E-18	-2.1171	0.3496	1.48E-09	-0.1133	0.0142	1.43E-15	1
rs34018943	17	43508303	17	43399058	44874453	A	G	0.1938	ARHGAP27	intronic	2.0482	0.2369	5.27E-18	2.1144	0.3492	1.49E-09	0.1133	0.0142	1.35E-15	1
rs34104358	17	43508616	17	43399058	44874453	T	G	0.1938	ARHGAP27	intronic	-2.0477	0.2367	5.08E-18	-2.1161	0.3492	1.45E-09	-0.1132	0.0142	1.43E-15	1
rs62064652	17	43509310	17	43399058	44874453	A	G	0.1928	ARHGAP27	intronic	2.0797	0.244	1.56E-17	2.1196	0.3492	1.36E-09	0.1185	0.0148	1.20E-15	1
rs62064653	17	43509316	17	43399058	44874453	T	C	0.1928	ARHGAP27	intronic	-2.0588	0.2385	6.09E-18	-2.1196	0.3492	1.36E-09	-0.1147	0.0144	1.71E-15	1
rs56020833	17	43509778	17	43399058	44874453	T	C	0.1938	ARHGAP27	intronic	-2.0401	0.2387	1.27E-17	-2.1149	0.3494	1.51E-09	-0.1137	0.0142	1.12E-15	1
rs55642947	17	43510187	17	43399058	44874453	C	G	0.1938	ARHGAP27	UTR5	-2.0607	0.2386	5.72E-18	-2.1169	0.3494	1.46E-09	-0.1156	0.0140	1.91E-16	1
rs34465449	17	43511435	17	43399058	44874453	A	C	0.1938	ARHGAP27	intronic	-1.9944	0.1843	2.68E-27	-2.1249	0.3494	1.26E-09	-0.1136	0.0142	1.04E-15	1
rs12946900	17	43512206	17	43399058	44874453	A	G	0.1938	ARHGAP27	upstream	1.9811	0.1842	5.74E-27	2.1347	0.3493	1.05E-09	0.1154	0.0140	1.77E-16	1
rs56168933	17	43512318	17	43399058	44874453	A	G	0.1938	ARHGAP27	upstream:downstre	-2.0304	0.1856	7.66E-28	-2.1351	0.3493	1.04E-09	-0.1153	0.0142	5.79E-16	1
rs55790407	17	43512439	17	43399058	44874453	C	G	0.1938	ARHGAP27	upstream:downstre	-1.9814	0.1843	5.73E-27	-2.1371	0.3493	1.01E-09	-0.1153	0.0140	1.82E-16	1
rs11012	17	43513441	17	43399058	44874453	T	C	0.1948	PLEKHM1	UTR3	-1.9828	0.184	4.48E-27	-2.1405	0.3493	9.47E-10	-0.1157	0.0140	1.39E-16	1
rs9730	17	43513551	17	43399058	44874453	C	G	0.1938	PLEKHM1	UTR3	1.9820	0.1842	5.42E-27	2.1414	0.3493	9.32E-10	0.1153	0.0140	1.84E-16	1
rs62064654	17	43513896	17	43399058	44874453	T	C	0.1938	PLEKHM1	UTR3	-1.9883	0.1852	6.69E-27	-2.1317	0.3495	1.12E-09	-0.1155	0.0140	1.90E-16	1
rs62064655	17	43514954	17	43399058	44874453	A	G	0.1938	PLEKHM1	UTR3	-2.0297	0.2362	8.34E-18	-2.1406	0.3493	9.44E-10	-0.1158	0.0140	1.59E-16	1
NA	17	43515846	17	43399058	44874453	T	C	0.1938	PLEKHM1	intronic	-2.0105	0.267	5.05E-14	-2.1367	0.3540	1.67E-09	-0.1158	0.0140	1.67E-16	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs36114997	17	43515885	17	43399058	44874453	A	G	0.1938	PLEKHM1	intronic	2.0291	0.2365	9.49E-18	2.1416	0.3493	9.27E-10	0.1158	0.0140	1.64E-16	1
rs568655892	17	43515927	17	43399058	44874453	T	C	0.1948	PLEKHM1	intronic	-2.0261	0.2361	9.37E-18	-2.1416	0.3493	9.27E-10	-0.1156	0.0141	2.12E-16	1
rs17631303	17	43516402	17	43399058	44874453	A	G	0.1938	PLEKHM1	intronic	1.9763	0.1848	1.11E-26	2.1348	0.3494	1.06E-09	0.1168	0.0141	1.08E-16	1
NA	17	43516739	17	43399058	44874453	A	G	0.1938	PLEKHM1	intronic	-2.0653	0.2706	2.33E-14	-2.1534	0.3498	7.94E-10	-0.1176	0.0142	1.52E-16	1
rs62064657	17	43517054	17	43399058	44874453	A	G	0.1938	PLEKHM1	intronic	-2.0409	0.2382	1.05E-17	-2.1375	0.3494	1.01E-09	-0.1167	0.0141	1.25E-16	1
rs35489312	17	43517252	17	43399058	44874453	T	C	0.1938	PLEKHM1	intronic	1.9734	0.1843	9.41E-27	2.1452	0.3493	8.70E-10	0.1166	0.0141	1.30E-16	1
NA	17	43519564	17	43399058	44874453	A	C	0.1938	PLEKHM1	intronic	-2.0102	0.2674	5.56E-14	-2.1445	0.3498	9.33E-10	-0.1169	0.0141	1.25E-16	1
rs62065374	17	43520272	17	43399058	44874453	A	G	0.1938	PLEKHM1	intronic	-2.0427	0.2386	1.13E-17	-2.1438	0.3495	9.09E-10	-0.1170	0.0141	1.25E-16	1
rs62065376	17	43521161	17	43399058	44874453	C	G	0.1948	PLEKHM1	intronic	2.0413	0.2382	1.03E-17	2.1393	0.3495	9.84E-10	0.1173	0.0141	1.04E-16	1
rs62065377	17	43521193	17	43399058	44874453	A	G	0.1948	PLEKHM1	intronic	2.0992	0.2448	9.89E-18	2.1497	0.3493	8.04E-10	0.1206	0.0150	1.03E-15	1
rs62065378	17	43522361	17	43399058	44874453	T	C	0.1938	PLEKHM1	intronic	1.9910	0.1847	4.34E-27	2.1475	0.3494	8.42E-10	0.1178	0.0142	1.09E-16	1
rs113575082	17	43524526	17	43399058	44874453	T	C	0.1938	PLEKHM1	intronic	-2.0675	0.2355	1.64E-18	-2.1395	0.3495	9.88E-10	-0.1181	0.0142	8.25E-17	1
rs71373572	17	43525022	17	43399058	44874453	A	G	0.1938	PLEKHM1	intronic	-2.0574	0.2341	1.53E-18	-2.1541	0.3494	7.45E-10	-0.1181	0.0142	9.09E-17	1
rs62065379	17	43525365	17	43399058	44874453	T	C	0.1938	PLEKHM1	intronic	-2.0818	0.2362	1.19E-18	-2.1440	0.3496	9.12E-10	-0.1182	0.0142	8.84E-17	1
NA	17	43527025	17	43399058	44874453	T	C	0.1938	PLEKHM1	intronic	-2.0972	0.2714	1.11E-14	-2.1415	0.3500	1.00E-09	-0.1182	0.0142	8.25E-17	1
rs112538459	17	43527323	17	43399058	44874453	T	C	0.1938	PLEKHM1	intronic	-1.9999	0.1846	2.36E-27	-2.1557	0.3494	7.29E-10	-0.1181	0.0142	8.79E-17	1
rs2077606	17	43529293	17	43399058	44874453	A	G	0.1938	PLEKHM1	intronic	-2.0799	0.2373	1.88E-18	-2.1613	0.3494	6.56E-10	-0.1186	0.0142	7.75E-17	1
rs2960000	17	43534353	17	43399058	44874453	T	C	0.1978	PLEKHM1:AC0911	ncRNA_intronic	2.1462	0.2522	1.76E-17	2.0753	0.3483	2.69E-09	0.1249	0.0148	3.60E-17	1
rs62065385	17	43534694	17	43399058	44874453	T	C	0.1958	PLEKHM1:AC0911	ncRNA_intronic	-2.0975	0.2404	2.68E-18	-2.1603	0.3495	6.79E-10	-0.1199	0.0143	5.32E-17	1
rs55703888	17	43536408	17	43399058	44874453	T	C	0.1938	PLEKHM1:AC0911	ncRNA_intronic	-2.0886	0.2396	2.81E-18	-2.1695	0.3493	5.63E-10	-0.1198	0.0143	5.66E-17	1
rs56005713	17	43536743	17	43399058	44874453	T	C	0.1938	PLEKHM1:AC0911	ncRNA_intronic	-2.0125	0.1858	2.47E-27	-2.1698	0.3493	5.61E-10	-0.1200	0.0143	5.01E-17	1
rs111423688	17	43538523	17	43399058	44874453	A	G	0.1938	PLEKHM1:AC0911	ncRNA_intronic	-2.1113	0.242	2.64E-18	-2.1651	0.3495	6.20E-10	-0.1205	0.0143	4.14E-17	1
rs62065389	17	43538807	17	43399058	44874453	T	G	0.1938	PLEKHM1:AC0911	ncRNA_intronic	2.1054	0.2433	5.05E-18	2.1650	0.3495	6.20E-10	0.1209	0.0143	3.46E-17	1
NA	17	43538991	17	43399058	44874453	A	G	0.1938	PLEKHM1:AC0911	ncRNA_intronic	-2.1131	0.2783	3.13E-14	-2.1548	0.3499	7.78E-10	-0.1216	0.0144	3.41E-17	1
NA	17	43538993	17	43399058	44874453	C	G	0.1938	PLEKHM1:AC0911	ncRNA_intronic	-2.1278	0.2793	2.57E-14	-2.1548	0.3499	7.78E-10	-0.1217	0.0145	4.25E-17	1
NA	17	43539035	17	43399058	44874453	A	G	0.1938	PLEKHM1:AC0911	ncRNA_intronic	-2.1146	0.2785	3.13E-14	-2.1549	0.3499	7.76E-10	-0.1215	0.0144	3.39E-17	1
NA	17	43539437	17	43399058	44874453	C	G	0.1938	PLEKHM1:AC0911	ncRNA_intronic	2.3295	0.3204	3.56E-13	2.1447	0.3500	9.46E-10	0.1345	0.0161	7.08E-17	1
NA	17	43539723	17	43399058	44874453	T	C	0.1938	PLEKHM1:AC0911	ncRNA_intronic	-2.3142	0.3745	6.46E-10	-2.1554	0.3499	7.68E-10	NA	NA	NA	NA
rs77099723	17	43539968	17	43399058	44874453	A	G	0.1938	PLEKHM1:AC0911	ncRNA_intronic	-2.1333	0.2501	1.45E-17	-2.1739	0.3493	5.18E-10	-0.1234	0.0145	1.81E-17	1
NA	17	43540472	17	43399058	44874453	A	T	0.1938	PLEKHM1:AC0911	ncRNA_intronic	2.3531	0.3419	5.91E-12	2.1626	0.3531	9.61E-10	0.1349	0.0174	8.65E-15	1
rs2139890	17	43541627	17	43399058	44874453	A	C	0.1938	PLEKHM1	intronic	-2.0469	0.1879	1.27E-27	-2.1734	0.3493	5.24E-10	-0.1220	0.0144	2.63E-17	1
rs3946526	17	43541656	17	43399058	44874453	T	C	0.1938	PLEKHM1	intronic	-2.1552	0.2475	3.10E-18	-2.1638	0.3495	6.34E-10	-0.1235	0.0146	2.97E-17	1
NA	17	43544206	17	43399058	44874453	C	G	0.1958	PLEKHM1	intronic	-2.3996	0.3678	6.87E-11	-2.1601	0.3486	6.17E-10	-0.1463	0.0191	1.95E-14	1
rs55663797	17	43544379	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	-2.0504	0.1882	1.26E-27	-2.1607	0.3484	5.96E-10	-0.1220	0.0144	2.05E-17	1
rs1879581	17	43545893	17	43399058	44874453	T	C	0.1958	PLEKHM1	exonic	2.0594	0.1893	1.48E-27	2.1633	0.3485	5.72E-10	0.1186	0.0147	8.18E-16	1
NA	17	43546057	17	43399058	44874453	T	G	0.1958	PLEKHM1	intronic	-2.2274	0.2866	7.68E-15	-2.1539	0.3486	6.85E-10	-0.1184	0.0147	9.68E-16	1
rs55671319	17	43548424	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	2.0872	0.1934	3.67E-27	2.1564	0.3487	6.66E-10	0.1207	0.0153	2.84E-15	1
rs55652155	17	43548481	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	2.2426	0.256	1.97E-18	2.1669	0.3486	5.42E-10	0.1206	0.0153	2.93E-15	1
rs17631676	17	43549526	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	2.0748	0.1931	6.47E-27	2.1682	0.3486	5.33E-10	0.1214	0.0151	7.12E-16	1
rs149366495	17	43549608	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	-2.0695	0.1936	1.15E-26	-2.1610	0.3488	6.17E-10	-0.1219	0.0151	7.37E-16	1
rs2090847	17	43550107	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	2.0868	0.1949	9.63E-27	2.1688	0.3487	5.29E-10	0.1235	0.0154	1.18E-15	1
rs55746869	17	43551083	17	43399058	44874453	T	C	0.1958	PLEKHM1	intronic	-2.2435	0.2604	7.01E-18	-2.1574	0.3490	6.78E-10	-0.1256	0.0156	6.83E-16	1
rs12950965	17	43551151	17	43399058	44874453	C	G	0.1958	PLEKHM1	intronic	2.2886	0.2658	7.35E-18	2.1700	0.3487	5.21E-10	0.1276	0.0160	1.70E-15	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs56015792	17	43551321	17	43399058	44874453	C	G	0.1958	PLEKHM1	intronic	-2.2303	0.2578	5.04E-18	-2.1702	0.3487	5.19E-10	-0.1236	0.0153	7.58E-16	1
NA	17	43551523	17	43399058	44874453	T	C	0.1958	PLEKHM1	intronic	2.2841	0.304	5.77E-14	2.2021	0.3498	3.26E-10	0.1260	0.0157	1.01E-15	1
NA	17	43551546	17	43399058	44874453	T	C	0.1958	PLEKHM1	intronic	-2.2921	0.3047	5.38E-14	-2.1878	0.3500	4.36E-10	-0.1265	0.0157	8.76E-16	1
rs62065404	17	43551613	17	43399058	44874453	T	C	0.1958	PLEKHM1	intronic	-2.2357	0.2599	7.91E-18	-2.1705	0.3487	5.17E-10	-0.1268	0.0157	8.21E-16	1
rs71238846	17	43552537	17	43399058	44874453	A	G	0.1958	PLEKHM1	exonic	-2.2373	0.2602	8.09E-18	-2.1714	0.3488	5.11E-10	-0.1271	0.0158	8.11E-16	1
rs147243132	17	43552717	17	43399058	44874453	C	G	0.1958	PLEKHM1	exonic	-2.3170	0.2628	1.18E-18	-2.1716	0.3488	5.09E-10	-0.1281	0.0160	1.01E-15	1
rs12452273	17	43552921	17	43399058	44874453	T	C	0.1958	PLEKHM1	exonic	-2.3051	0.2637	2.27E-18	-2.1718	0.3488	5.08E-10	-0.1287	0.0161	1.29E-15	1
rs56192752	17	43555253	17	43399058	44874453	A	G	0.1958	PLEKHM1	UTR3	2.1184	0.196	3.18E-27	2.1736	0.3488	4.93E-10	0.1293	0.0161	8.69E-16	1
rs62065436	17	43556652	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	-2.3218	0.2686	5.42E-18	-2.1666	0.3490	5.72E-10	-0.1297	0.0162	1.09E-15	1
rs55925547	17	43556807	17	43399058	44874453	T	C	0.1978	PLEKHM1	intronic	2.3578	0.269	1.85E-18	2.1511	0.3480	6.77E-10	0.1316	0.0163	6.62E-16	1
NA	17	43556862	17	43399058	44874453	T	C	0.1958	PLEKHM1	intronic	-2.5074	0.3345	6.61E-14	-2.1530	0.3487	7.05E-10	-0.1341	0.0166	7.15E-16	1
rs55643511	17	43556982	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	-2.3190	0.2685	5.79E-18	-2.1740	0.3489	4.93E-10	-0.1313	0.0163	7.76E-16	1
rs62065437	17	43557612	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	-2.3195	0.2686	5.92E-18	-2.1742	0.3489	4.92E-10	-0.1314	0.0163	8.25E-16	1
rs62065438	17	43558092	17	43399058	44874453	T	C	0.1958	PLEKHM1	intronic	-2.1191	0.1993	2.10E-26	-2.1667	0.3490	5.73E-10	-0.1323	0.0164	6.90E-16	1
NA	17	43563093	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	2.5529	0.3565	7.96E-13	2.1622	0.3489	6.14E-10	0.1431	0.0176	5.13E-16	1
rs62065442	17	43563894	17	43399058	44874453	T	C	0.1958	PLEKHM1	intronic	2.3014	0.2859	8.29E-16	2.1761	0.3490	4.80E-10	0.1355	0.0169	1.25E-15	1
rs144733372	17	43564222	17	43399058	44874453	T	G	0.1958	PLEKHM1	intronic	2.2869	0.2865	1.45E-15	2.1747	0.3489	4.88E-10	0.1360	0.0170	1.13E-15	1
rs62065445	17	43565840	17	43399058	44874453	A	G	0.1958	PLEKHM1	intronic	-2.3002	0.2869	1.08E-15	-2.1791	0.3490	4.54E-10	-0.1368	0.0171	1.13E-15	1
rs1879585	17	43567175	17	43399058	44874453	T	G	0.1968	PLEKHM1	intronic	2.3038	0.2879	1.21E-15	2.1589	0.3493	6.77E-10	0.1379	0.0172	1.21E-15	1
NA	17	43568928	17	43399058	44874453	A	T	0.1958	PLEKHM1	upstream	-2.3919	0.3549	1.58E-11	-2.1487	0.3490	7.93E-10	-0.1414	0.0176	1.01E-15	1
NA	17	43569083	17	43399058	44874453	T	C	0.1988	PLEKHM1	upstream	-2.3911	0.3513	9.99E-12	-2.1430	0.3487	8.47E-10	-0.1403	0.0174	8.88E-16	1
rs113322852	17	43569245	17	43399058	44874453	A	T	0.1988	PLEKHM1	intergenic	-2.1015	0.2058	1.74E-24	-2.1731	0.3494	5.30E-10	-0.1369	0.0177	1.21E-14	1
rs62065448	17	43569770	17	43399058	44874453	T	C	0.1998	PLEKHM1	intergenic	-2.3205	0.2893	1.05E-15	-2.1505	0.3509	9.38E-10	-0.1371	0.0179	1.72E-14	1
rs62065449	17	43569909	17	43399058	44874453	T	C	0.1988	PLEKHM1	intergenic	2.3158	0.2886	1.02E-15	2.1598	0.3491	6.54E-10	0.1374	0.0180	2.01E-14	1
rs1879583	17	43570893	17	43399058	44874453	T	C	0.1988	PLEKHM1	intergenic	-2.1765	0.3035	7.41E-13	-2.1595	0.3491	6.57E-10	-0.1393	0.0187	9.34E-14	1
rs1724390	17	43663247	17	43399058	44874453	A	C	0.2435	DND1P1	ncRNA_exonic	-1.8194	0.2047	6.10E-19	-2.0648	0.3208	1.31E-10	NA	NA	NA	NA
rs117368197	17	43715924	17	43399058	44874453	A	G	0.2396	CRHR1-IT1:CRHR1	ncRNA_intronic	1.8520	0.1976	7.08E-21	2.2034	0.3214	7.80E-12	NA	NA	NA	NA
rs111273167	17	43740967	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.7940	0.1964	6.50E-20	-2.2033	0.3214	7.80E-12	NA	NA	NA	NA
rs112155389	17	43758078	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.8394	0.1957	5.43E-21	-2.2034	0.3214	7.80E-12	NA	NA	NA	NA
rs112431991	17	43758885	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.8499	0.1965	4.68E-21	2.1833	0.3233	1.58E-11	NA	NA	NA	NA
rs113661667	17	43791610	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.7881	0.1959	7.05E-20	2.2118	0.3216	6.71E-12	NA	NA	NA	NA
rs111415173	17	43795573	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.7533	0.196	3.73E-19	-2.2115	0.3216	6.75E-12	NA	NA	NA	NA
rs113991678	17	43795634	17	43399058	44874453	T	C	0.2386	CRHR1:RP11-105N	ncRNA_intronic	-1.7536	0.1961	3.81E-19	-2.2115	0.3216	6.75E-12	NA	NA	NA	NA
rs112995313	17	43795768	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.7436	0.1961	5.96E-19	2.2115	0.3216	6.75E-12	NA	NA	NA	NA
rs117615688	17	43798308	17	43399058	44874453	A	G	0.07058	CRHR1:RP11-105N	ncRNA_intronic	-1.9423	0.3549	4.43E-08	-1.9337	0.5391	3.37E-04	NA	NA	NA	NA
rs112570965	17	43801092	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.7962	0.1962	5.36E-20	2.2111	0.3216	6.80E-12	NA	NA	NA	NA
rs113790915	17	43810782	17	43399058	44874453	C	G	0.2396	CRHR1:RP11-105N	ncRNA_exonic	-1.8211	0.1952	1.06E-20	-2.2124	0.3216	6.59E-12	NA	NA	NA	NA
rs62055869	17	43830685	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.7872	0.1947	4.35E-20	-2.2130	0.3216	6.49E-12	NA	NA	NA	NA
rs17426174	17	43830938	17	43399058	44874453	C	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.7870	0.1947	4.39E-20	-2.2135	0.3216	6.42E-12	NA	NA	NA	NA
rs62055885	17	43838014	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.0658	0.2631	4.07E-15	2.2165	0.3217	6.15E-12	0.1214	0.0181	1.88E-11	1
rs28439278	17	43838071	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.0653	0.263	4.12E-15	-2.2147	0.3216	6.28E-12	-0.1213	0.0181	1.88E-11	1
rs12150621	17	43838482	17	43399058	44874453	T	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.0640	0.2627	3.89E-15	-2.2146	0.3216	6.33E-12	-0.1185	0.0178	3.06E-11	1
rs62055886	17	43838678	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.0627	0.2631	4.48E-15	-2.2080	0.3218	7.47E-12	-0.1183	0.0178	3.13E-11	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs62055887	17	43838710	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.0626	0.2631	4.48E-15	2.2080	0.3218	7.49E-12	0.1213	0.0176	5.73E-12	1
rs62055888	17	43838720	17	43399058	44874453	T	C	0.2366	CRHR1:RP11-105N	ncRNA_intronic	-2.0513	0.2644	8.58E-15	-2.1850	0.3243	1.76E-11	-0.1193	0.0176	1.16E-11	1
rs62055889	17	43838919	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.0635	0.2635	4.85E-15	-2.2147	0.3216	6.30E-12	-0.1221	0.0174	2.09E-12	1
rs71375313	17	43839253	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.0607	0.263	4.64E-15	-2.2183	0.3219	6.06E-12	-0.1219	0.0173	2.05E-12	1
rs11079718	17	43839951	17	43399058	44874453	A	T	0.2435	CRHR1:RP11-105N	ncRNA_intronic	2.2439	0.2612	8.74E-18	2.2498	0.3222	3.20E-12	0.1243	0.0176	1.68E-12	1
rs11079719	17	43840006	17	43399058	44874453	T	G	0.2435	CRHR1:RP11-105N	ncRNA_intronic	2.1870	0.2595	3.54E-17	2.2218	0.3239	7.56E-12	0.1227	0.0175	2.65E-12	1
rs11079720	17	43840016	17	43399058	44874453	A	G	0.2386	CRHR1:RP11-105N	ncRNA_intronic	-2.1530	0.2593	1.02E-16	-2.1971	0.3243	1.35E-11	-0.1211	0.0172	1.74E-12	1
rs11079721	17	43840107	17	43399058	44874453	A	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1517	0.2585	8.59E-17	-2.2300	0.3219	4.73E-12	-0.1233	0.0169	2.94E-13	1
rs62055890	17	43840681	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1538	0.2585	7.89E-17	-2.2137	0.3217	6.47E-12	-0.1227	0.0168	3.19E-13	1
rs77849344	17	43840864	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1510	0.2583	8.20E-17	-2.2177	0.3217	5.99E-12	-0.1220	0.0167	3.08E-13	1
rs74918686	17	43840899	17	43399058	44874453	C	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1511	0.2582	8.09E-17	-2.2178	0.3217	6.00E-12	-0.1220	0.0167	3.09E-13	1
rs79545140	17	43840935	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1506	0.2582	8.24E-17	2.2172	0.3217	6.08E-12	0.1223	0.0167	2.14E-13	1
rs56369036	17	43841571	17	43399058	44874453	A	T	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1454	0.2581	9.28E-17	-2.2146	0.3217	6.37E-12	-0.1219	0.0166	2.22E-13	1
rs11079723	17	43841729	17	43399058	44874453	T	C	0.2406	CRHR1:RP11-105N	ncRNA_intronic	2.1456	0.258	9.18E-17	2.2056	0.3217	7.79E-12	0.1219	0.0167	2.91E-13	1
rs11079724	17	43841912	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1421	0.2578	9.52E-17	-2.2155	0.3217	6.23E-12	-0.1219	0.0166	2.12E-13	1
rs55707339	17	43842462	17	43399058	44874453	T	C	0.2406	CRHR1:RP11-105N	ncRNA_intronic	2.1336	0.2578	1.26E-16	2.1980	0.3220	9.51E-12	0.1217	0.0166	2.17E-13	1
rs62055893	17	43842494	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1328	0.2577	1.28E-16	2.2039	0.3219	8.32E-12	0.1216	0.0166	2.14E-13	1
rs75257002	17	43843395	17	43399058	44874453	T	C	0.2406	CRHR1:RP11-105N	ncRNA_intronic	-2.1332	0.2577	1.26E-16	-2.2151	0.3220	6.66E-12	-0.1211	0.0165	2.38E-13	1
rs62055894	17	43843943	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1304	0.2576	1.35E-16	-2.2215	0.3217	5.46E-12	-0.1211	0.0165	2.34E-13	1
rs62055895	17	43844044	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1315	0.2576	1.28E-16	2.2228	0.3216	5.29E-12	0.1211	0.0165	2.36E-13	1
rs62055896	17	43844201	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1315	0.2577	1.31E-16	-2.2228	0.3216	5.29E-12	-0.1209	0.0165	2.41E-13	1
rs55725840	17	43844486	17	43399058	44874453	A	T	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1315	0.2575	1.27E-16	-2.2228	0.3216	5.29E-12	-0.1208	0.0165	2.24E-13	1
rs56194509	17	43844559	17	43399058	44874453	T	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1647	0.2605	9.56E-17	2.2337	0.3248	6.66E-12	0.1218	0.0167	3.10E-13	1
rs55657917	17	43844560	17	43399058	44874453	T	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1650	0.2609	1.05E-16	2.2337	0.3248	6.67E-12	0.1221	0.0166	2.16E-13	1
rs56082319	17	43844798	17	43399058	44874453	A	G	0.2406	CRHR1:RP11-105N	ncRNA_intronic	-2.1333	0.2573	1.11E-16	-2.2169	0.3217	6.04E-12	-0.1200	0.0164	2.45E-13	1
rs56109643	17	43844859	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1321	0.2572	1.15E-16	2.2227	0.3216	5.29E-12	0.1227	0.0162	3.49E-14	1
rs62055899	17	43844977	17	43399058	44874453	A	T	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1324	0.2572	1.14E-16	-2.2244	0.3217	5.19E-12	-0.1225	0.0162	3.49E-14	1
rs62055900	17	43845002	17	43399058	44874453	C	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1322	0.2572	1.14E-16	2.2246	0.3217	5.16E-12	0.1225	0.0162	3.44E-14	1
rs62055901	17	43845041	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1321	0.2572	1.14E-16	-2.2164	0.3216	6.04E-12	-0.1225	0.0162	3.43E-14	1
rs58089049	17	43845480	17	43399058	44874453	T	C	0.2883	CRHR1:RP11-105N	ncRNA_intronic	-1.6212	0.2353	5.62E-12	-1.6788	0.3032	3.21E-08	-0.0926	0.0167	3.02E-08	1
rs62055903	17	43846668	17	43399058	44874453	A	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1310	0.257	1.11E-16	-2.2227	0.3216	5.29E-12	-0.1220	0.0161	3.47E-14	1
rs111374028	17	43846820	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1309	0.257	1.12E-16	-2.2228	0.3216	5.28E-12	-0.1218	0.0161	3.45E-14	1
rs113934115	17	43847039	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1645	0.2594	7.24E-17	-2.2228	0.3216	5.28E-12	-0.1239	0.0163	2.52E-14	1
NA	17	43847095	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1207	0.3085	6.20E-12	-2.2286	0.3217	4.72E-12	-0.1216	0.0160	3.31E-14	1
rs62055928	17	43847374	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1339	0.2571	1.03E-16	-2.2229	0.3216	5.28E-12	-0.1210	0.0160	4.26E-14	1
rs56268325	17	43847741	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1303	0.2569	1.12E-16	2.2228	0.3216	5.28E-12	0.1211	0.0160	3.25E-14	1
rs56070245	17	43847868	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1396	0.2522	2.18E-17	2.2228	0.3216	5.28E-12	0.1211	0.0160	3.28E-14	1
rs56387266	17	43847912	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1397	0.2522	2.16E-17	2.2228	0.3216	5.28E-12	0.1211	0.0159	3.18E-14	1
rs34303488	17	43848181	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1397	0.2522	2.15E-17	-2.2227	0.3216	5.30E-12	-0.1209	0.0159	3.19E-14	1
rs62055932	17	43848412	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1431	0.2517	1.66E-17	2.2118	0.3216	6.69E-12	0.1208	0.0159	3.17E-14	1
rs62055933	17	43848461	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1214	0.2543	7.36E-17	-2.2407	0.3220	3.78E-12	-0.1211	0.0159	2.82E-14	1
NA	17	43848638	17	43399058	44874453	A	G	0.2386	CRHR1:RP11-105N	ncRNA_intronic	-2.1272	0.3117	8.82E-12	-2.2823	0.3227	1.68E-12	-0.1217	0.0161	3.91E-14	1
rs62055935	17	43848750	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1369	0.2529	2.94E-17	2.2681	0.3235	2.60E-12	0.1211	0.0159	2.93E-14	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs62055936	17	43848761	17	43399058	44874453	A	T	0.2406	CRHR1:RP11-105N	ncRNA_intronic	-2.1367	0.2528	2.88E-17	-2.2671	0.3234	2.61E-12	-0.1208	0.0159	3.34E-14	1
rs62055937	17	43848968	17	43399058	44874453	T	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1444	0.2521	1.80E-17	-2.2494	0.3223	3.27E-12	-0.1204	0.0158	3.03E-14	1
rs76294809	17	43849327	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1376	0.252	2.22E-17	-2.2207	0.3216	5.52E-12	-0.1206	0.0158	2.70E-14	1
rs75916678	17	43849366	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1384	0.252	2.17E-17	2.2160	0.3217	6.17E-12	0.1205	0.0158	2.69E-14	1
rs79730878	17	43849415	17	43399058	44874453	T	C	0.2455	CRHR1:RP11-105N	ncRNA_intronic	2.1374	0.2553	5.59E-17	2.1507	0.3198	1.90E-11	0.1189	0.0150	2.58E-15	1
rs62055938	17	43849656	17	43399058	44874453	A	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1389	0.2518	1.97E-17	-2.2229	0.3216	5.27E-12	-0.1200	0.0158	2.77E-14	1
rs62055939	17	43849787	17	43399058	44874453	A	T	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1384	0.2517	1.99E-17	2.2229	0.3216	5.27E-12	0.1201	0.0154	7.20E-15	1
rs62055940	17	43849896	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1386	0.2517	1.94E-17	2.2229	0.3216	5.27E-12	0.1201	0.0154	7.08E-15	1
rs76885724	17	43850519	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1379	0.2516	1.96E-17	-2.2229	0.3216	5.27E-12	-0.1201	0.0154	6.96E-15	1
rs60814418	17	43850645	17	43399058	44874453	T	C	0.2435	CRHR1:RP11-105N	ncRNA_intronic	-2.0436	0.2493	2.47E-16	-2.2215	0.3205	4.60E-12	-0.1197	0.0158	3.61E-14	1
NA	17	43850932	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1178	0.3169	2.33E-11	-2.2290	0.3217	4.67E-12	-0.1192	0.0163	2.66E-13	1
rs62055942	17	43850966	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1415	0.252	1.93E-17	2.2229	0.3216	5.28E-12	0.1199	0.0154	6.92E-15	1
rs62055943	17	43851018	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1398	0.251	1.52E-17	2.2228	0.3216	5.28E-12	0.1197	0.0154	7.09E-15	1
rs62055945	17	43851851	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1368	0.2514	1.92E-17	-2.2228	0.3216	5.29E-12	-0.1169	0.0149	4.20E-15	1
rs62055946	17	43851971	17	43399058	44874453	A	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1365	0.2514	1.93E-17	-2.2231	0.3216	5.25E-12	-0.1166	0.0149	4.43E-15	1
rs62055947	17	43852605	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1374	0.2519	2.15E-17	-2.2265	0.3228	5.80E-12	-0.1165	0.0149	4.49E-15	1
rs62055948	17	43852621	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1373	0.2518	2.10E-17	2.2260	0.3228	5.85E-12	0.1164	0.0148	4.48E-15	1
rs113871181	17	43852733	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9957	0.1853	4.74E-27	-2.2135	0.3223	7.13E-12	-0.1163	0.0148	4.59E-15	1
rs111370985	17	43852742	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9961	0.1853	4.63E-27	2.2072	0.3223	8.24E-12	0.1163	0.0148	4.48E-15	1
rs55787105	17	43853109	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1353	0.2513	1.92E-17	-2.2231	0.3216	5.26E-12	-0.1164	0.0148	4.10E-15	1
rs62055950	17	43853133	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1350	0.2512	1.93E-17	2.2227	0.3216	5.29E-12	0.1162	0.0148	4.34E-15	1
rs56043078	17	43853235	17	43399058	44874453	T	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1348	0.2512	1.90E-17	2.2227	0.3216	5.29E-12	0.1161	0.0148	4.35E-15	1
rs77965652	17	43853457	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1346	0.2512	1.91E-17	2.2227	0.3216	5.29E-12	0.1160	0.0148	4.47E-15	1
rs55849949	17	43853526	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1345	0.2511	1.91E-17	2.2228	0.3216	5.28E-12	0.1161	0.0148	4.31E-15	1
rs56303031	17	43853922	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.0659	0.2792	1.37E-13	-2.2181	0.3216	5.87E-12	-0.1160	0.0148	4.00E-15	1
rs55991914	17	43854267	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1345	0.2511	1.91E-17	-2.2228	0.3216	5.28E-12	-0.1158	0.0147	3.83E-15	1
rs62055955	17	43854340	17	43399058	44874453	A	G	0.2406	CRHR1:RP11-105N	ncRNA_intronic	2.1327	0.2511	2.01E-17	2.2239	0.3215	5.09E-12	0.1156	0.0147	4.21E-15	1
rs62055956	17	43854449	17	43399058	44874453	T	C	0.2406	CRHR1:RP11-105N	ncRNA_intronic	-2.1399	0.2511	1.58E-17	-2.2303	0.3215	4.41E-12	-0.1156	0.0147	4.09E-15	1
rs12938031	17	43854502	17	43399058	44874453	A	G	0.3887	CRHR1:RP11-105N	ncRNA_intronic	1.1816	0.2108	2.08E-08	1.6389	0.2714	1.64E-09	0.0458	0.0125	2.42E-04	1
rs62055957	17	43854536	17	43399058	44874453	A	C	0.2406	CRHR1:RP11-105N	ncRNA_intronic	-2.1334	0.2511	1.95E-17	-2.2240	0.3215	5.08E-12	-0.1155	0.0147	4.10E-15	1
rs4074462	17	43855228	17	43399058	44874453	T	G	0.2406	CRHR1:RP11-105N	ncRNA_intronic	-2.1157	0.2501	2.71E-17	-2.2180	0.3215	5.78E-12	-0.1153	0.0147	4.31E-15	1
rs574201100	17	43855603	17	43399058	44874453	A	G	0.3926	CRHR1:RP11-105N	ncRNA_intronic	-1.1837	0.2105	1.87E-08	-1.5945	0.2708	4.14E-09	-0.0487	0.0130	1.82E-04	1
NA	17	43856372	17	43399058	44874453	A	G	0.2386	CRHR1:RP11-105N	ncRNA_intronic	-2.1170	0.2964	9.26E-13	-2.2455	0.3232	4.07E-12	-0.1144	0.0141	5.16E-16	1
rs62057061	17	43856639	17	43399058	44874453	C	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.1370	0.2496	1.12E-17	2.2126	0.3219	6.83E-12	0.1142	0.0141	5.02E-16	1
rs62057062	17	43856710	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9869	0.1843	4.22E-27	-2.2227	0.3216	5.30E-12	-0.1142	0.0141	5.02E-16	1
rs62057063	17	43856730	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9914	0.1848	4.49E-27	-2.2323	0.3219	4.48E-12	-0.1153	0.0142	4.94E-16	1
rs62057064	17	43857033	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9859	0.183	1.90E-27	-2.2228	0.3216	5.30E-12	-0.1141	0.0141	5.07E-16	1
rs76830096	17	43857129	17	43399058	44874453	A	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9820	0.183	2.40E-27	2.2227	0.3216	5.29E-12	0.1140	0.0141	5.11E-16	1
rs62057065	17	43858187	17	43399058	44874453	T	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.1329	0.251	1.91E-17	-2.2128	0.3217	6.60E-12	-0.1144	0.0141	5.42E-16	1
NA	17	43858307	17	43399058	44874453	T	C	0.2406	CRHR1:RP11-105N	ncRNA_intronic	2.1086	0.3031	3.48E-12	2.2364	0.3231	4.92E-12	0.1150	0.0143	7.17E-16	1
rs62057067	17	43858326	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9871	0.1847	5.58E-27	-2.2218	0.3216	5.39E-12	-0.1150	0.0142	5.38E-16	1
rs78917495	17	43858482	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9812	0.1828	2.30E-27	-2.2154	0.3216	6.22E-12	-0.1131	0.0140	5.27E-16	1
rs62057068	17	43858629	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9810	0.1828	2.31E-27	2.2215	0.3216	5.42E-12	0.1130	0.0139	5.16E-16	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs62057069	17	43859065	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9806	0.1828	2.36E-27	2.2209	0.3216	5.47E-12	0.1131	0.0139	4.72E-16	1
rs62057070	17	43859640	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9806	0.1828	2.33E-27	2.2210	0.3216	5.46E-12	0.1126	0.0139	4.80E-16	1
rs62057071	17	43859691	17	43399058	44874453	C	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9804	0.1828	2.37E-27	2.2210	0.3216	5.45E-12	0.1125	0.0139	5.00E-16	1
rs62057073	17	43861117	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9866	0.1851	7.08E-27	-2.2536	0.3221	2.91E-12	-0.1136	0.0141	9.45E-16	1
rs12944712	17	43871147	17	43399058	44874453	A	G	0.4682	CRHR1:RP11-105N	ncRNA_intronic	-0.9449	0.1438	4.99E-11	-1.3643	0.2672	3.41E-07	-0.0328	0.0106	2.06E-03	1
rs56319902	17	43871982	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.0011	0.1821	4.19E-28	-2.2227	0.3220	5.62E-12	-0.1102	0.0136	4.30E-16	1
rs55943044	17	43872228	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9906	0.1821	8.00E-28	-2.2187	0.3216	5.74E-12	-0.1099	0.0135	4.83E-16	1
rs80184151	17	43879308	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9699	0.1808	1.21E-27	2.2310	0.3214	4.25E-12	0.1089	0.0134	4.38E-16	1
rs17689378	17	43881790	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9418	0.1802	4.34E-27	-2.2310	0.3214	4.25E-12	-0.1086	0.0133	4.05E-16	1
rs62057101	17	43885291	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9399	0.1801	4.77E-27	-2.2298	0.3214	4.39E-12	-0.1087	0.0133	3.28E-16	1
rs62057103	17	43887480	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.0545	0.2396	1.00E-17	2.2289	0.3216	4.59E-12	0.1093	0.0133	2.12E-16	1
rs55915917	17	43892784	17	43399058	44874453	T	G	0.2256	CRHR1:RP11-105N	ncRNA_intronic	2.0065	0.1846	1.66E-27	2.2602	0.3244	3.56E-12	0.1135	0.0138	2.23E-16	1
rs55668363	17	43892788	17	43399058	44874453	A	G	0.2247	CRHR1:RP11-105N	ncRNA_intronic	-1.9993	0.1848	2.79E-27	-2.2555	0.3248	4.17E-12	-0.1129	0.0138	3.67E-16	1
rs17689471	17	43892973	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9470	0.1799	2.73E-27	2.2382	0.3214	3.66E-12	0.1092	0.0132	1.69E-16	1
rs117365970	17	43893259	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-2.0072	0.1836	7.92E-28	-2.2534	0.3221	2.92E-12	-0.1144	0.0139	2.11E-16	1
rs117646503	17	43893260	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	2.0258	0.1831	1.94E-28	2.2385	0.3214	3.66E-12	0.1150	0.0139	1.35E-16	1
rs17762769	17	43893403	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9477	0.1799	2.59E-27	-2.2386	0.3215	3.64E-12	-0.1093	0.0132	1.54E-16	1
rs8072451	17	43893716	17	43399058	44874453	T	C	0.2396	CRHR1:RP11-105N	ncRNA_intronic	-1.9544	0.1799	1.69E-27	-2.2398	0.3221	3.90E-12	-0.1093	0.0132	1.54E-16	1
rs8073146	17	43893751	17	43399058	44874453	A	G	0.2396	CRHR1:RP11-105N	ncRNA_intronic	1.9523	0.1799	1.95E-27	2.2434	0.3223	3.71E-12	0.1093	0.0132	1.57E-16	1
rs28364025	17	43894102	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9486	0.1799	2.46E-27	2.2413	0.3216	3.50E-12	0.1093	0.0132	1.50E-16	1
rs28364023	17	43894159	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9495	0.18	2.46E-27	-2.2403	0.3216	3.58E-12	-0.1092	0.0132	1.55E-16	1
rs55779147	17	43894510	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9519	0.1801	2.31E-27	-2.2414	0.3215	3.44E-12	-0.1097	0.0133	1.48E-16	1
rs56357543	17	43894547	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9497	0.1802	2.69E-27	-2.2539	0.3217	2.70E-12	-0.1097	0.0133	1.48E-16	1
rs56099546	17	43894609	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9498	0.1802	2.68E-27	2.2541	0.3217	2.69E-12	0.1097	0.0133	1.48E-16	1
rs739645	17	43894990	17	43399058	44874453	T	G	0.2396	CRHR1	intronic	1.9532	0.1802	2.18E-27	2.2428	0.3215	3.35E-12	0.1096	0.0133	1.56E-16	1
rs739644	17	43895008	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	1.9519	0.1801	2.31E-27	2.2427	0.3215	3.35E-12	0.1096	0.0133	1.54E-16	1
rs4564621	17	43895501	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	-1.9523	0.1802	2.32E-27	-2.2443	0.3215	3.25E-12	-0.1095	0.0133	1.59E-16	1
rs2316763	17	43895530	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9717	0.1801	6.89E-28	-2.2458	0.3216	3.17E-12	-0.1100	0.0133	1.15E-16	1
rs2316764	17	43895602	17	43399058	44874453	T	G	0.2396	CRHR1	intronic	1.9426	0.18	3.63E-27	2.2370	0.3216	3.87E-12	0.1090	0.0132	1.63E-16	1
rs4277389	17	43895653	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9455	0.1801	3.28E-27	2.2356	0.3216	3.96E-12	0.1096	0.0132	1.14E-16	1
rs4566211	17	43895696	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9526	0.18	2.10E-27	-2.2464	0.3216	3.13E-12	-0.1090	0.0132	1.58E-16	1
rs4566212	17	43895751	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9525	0.18	2.10E-27	-2.2462	0.3215	3.12E-12	-0.1090	0.0132	1.58E-16	1
rs4309444	17	43895797	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9478	0.1801	2.86E-27	2.2372	0.3216	3.84E-12	0.1090	0.0132	1.58E-16	1
rs62057107	17	43896032	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9597	0.18	1.33E-27	-2.2355	0.3215	3.96E-12	-0.1092	0.0132	1.61E-16	1
rs12150390	17	43896228	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9609	0.1799	1.15E-27	2.2446	0.3215	3.21E-12	0.1091	0.0132	1.51E-16	1
rs17689608	17	43896528	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	1.9585	0.1797	1.20E-27	2.2358	0.3215	3.93E-12	0.1091	0.0132	1.47E-16	1
rs62057108	17	43896616	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9562	0.1799	1.57E-27	2.2359	0.3215	3.93E-12	0.1091	0.0132	1.51E-16	1
rs62057109	17	43896637	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9561	0.1799	1.58E-27	2.2359	0.3215	3.93E-12	0.1091	0.0132	1.50E-16	1
rs78074121	17	43896690	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9563	0.1799	1.53E-27	2.2379	0.3216	3.77E-12	0.1091	0.0132	1.49E-16	1
rs62057110	17	43896734	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9549	0.18	1.77E-27	2.2359	0.3215	3.92E-12	0.1092	0.0132	1.50E-16	1
rs62057111	17	43897130	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9499	0.1799	2.19E-27	2.2420	0.3214	3.33E-12	0.1091	0.0132	1.40E-16	1
rs62057112	17	43897202	17	43399058	44874453	A	T	0.2396	CRHR1	intronic	-1.9520	0.1798	1.92E-27	-2.2496	0.3215	2.88E-12	-0.1092	0.0132	1.36E-16	1
rs78587102	17	43897246	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9543	0.1797	1.47E-27	2.2495	0.3215	2.89E-12	0.1092	0.0132	1.32E-16	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs62057113	17	43897449	17	43399058	44874453	A	T	0.2396	CRHR1	intronic	1.9866	0.1811	5.32E-28	2.2363	0.3216	3.89E-12	0.1109	0.0133	8.92E-17	1
rs78506181	17	43897480	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9838	0.181	6.07E-28	2.2454	0.3215	3.16E-12	0.1109	0.0133	8.90E-17	1
rs79600142	17	43897722	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9856	0.1811	5.54E-28	2.2368	0.3217	3.93E-12	0.1109	0.0133	8.82E-17	1
rs111739681	17	43898459	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9508	0.1799	2.12E-27	-2.2282	0.3217	4.78E-12	-0.1093	0.0132	1.25E-16	1
rs17762882	17	43898887	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9494	0.1799	2.26E-27	2.2357	0.3216	3.96E-12	0.1093	0.0132	1.23E-16	1
rs17689653	17	43898963	17	43399058	44874453	A	T	0.2396	CRHR1	intronic	1.9495	0.1799	2.23E-27	2.2357	0.3216	3.96E-12	0.1093	0.0132	1.23E-16	1
rs17762912	17	43899161	17	43399058	44874453	A	C	0.2396	CRHR1	intronic	1.9501	0.1799	2.21E-27	2.2406	0.3217	3.62E-12	0.1093	0.0132	1.21E-16	1
rs62057114	17	43899401	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9507	0.1799	2.13E-27	-2.2380	0.3216	3.79E-12	-0.1093	0.0132	1.20E-16	1
rs62057115	17	43899417	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	-1.9492	0.1799	2.30E-27	-2.2380	0.3216	3.79E-12	-0.1093	0.0132	1.19E-16	1
rs78917479	17	43899611	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9492	0.1799	2.29E-27	-2.2380	0.3216	3.78E-12	-0.1093	0.0132	1.17E-16	1
rs62057116	17	43899655	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9496	0.1799	2.23E-27	2.2382	0.3216	3.79E-12	0.1093	0.0132	1.19E-16	1
rs62057117	17	43899657	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	1.9497	0.1799	2.22E-27	2.2385	0.3216	3.76E-12	0.1093	0.0132	1.16E-16	1
rs62057118	17	43899727	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9498	0.1799	2.31E-27	2.2487	0.3217	3.05E-12	0.1093	0.0132	1.13E-16	1
rs62057119	17	43899736	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9468	0.1799	2.71E-27	-2.2475	0.3217	3.11E-12	-0.1093	0.0132	1.12E-16	1
rs17762954	17	43899786	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9468	0.1799	2.71E-27	-2.2473	0.3217	3.11E-12	-0.1093	0.0132	1.12E-16	1
NA	17	43900081	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-2.0190	0.2787	4.35E-13	-2.2321	0.3217	4.39E-12	-0.1093	0.0132	1.11E-16	1
rs55638417	17	43900434	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	2.0678	0.2408	8.92E-18	2.2400	0.3216	3.61E-12	0.1109	0.0133	6.40E-17	1
rs79501144	17	43900697	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9479	0.1798	2.41E-27	-2.2381	0.3216	3.75E-12	-0.1093	0.0132	1.11E-16	1
NA	17	43900760	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-2.0175	0.2827	9.62E-13	-2.2535	0.3253	4.74E-12	-0.1114	0.0135	1.29E-16	1
rs112137135	17	43900817	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	2.0711	0.2396	5.35E-18	2.2384	0.3216	3.73E-12	0.1102	0.0133	1.12E-16	1
rs62057122	17	43901001	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9504	0.1796	1.77E-27	-2.2376	0.3216	3.82E-12	-0.1098	0.0132	8.60E-17	1
rs173365	17	43901074	17	43399058	44874453	A	G	0.4433	CRHR1	intronic	-0.8810	0.1404	3.54E-10	-1.1331	0.2736	3.50E-05	-0.0537	0.0110	1.16E-06	1
rs62057123	17	43901238	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9481	0.1798	2.38E-27	2.2381	0.3216	3.75E-12	0.1093	0.0132	1.08E-16	1
rs62057143	17	43901528	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9528	0.1798	1.74E-27	2.2475	0.3215	3.03E-12	0.1094	0.0132	1.06E-16	1
rs62057144	17	43901558	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9579	0.1799	1.34E-27	2.2457	0.3215	3.15E-12	0.1089	0.0132	1.58E-16	1
rs4335809	17	43902216	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9531	0.1798	1.73E-27	-2.2473	0.3215	3.04E-12	-0.1094	0.0132	1.05E-16	1
rs4341787	17	43902505	17	43399058	44874453	T	C	0.2406	CRHR1	intronic	-1.9531	0.1798	1.73E-27	-2.2471	0.3215	3.06E-12	-0.1094	0.0132	1.04E-16	1
rs4523962	17	43902522	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9531	0.1798	1.74E-27	-2.2471	0.3215	3.06E-12	-0.1094	0.0132	1.04E-16	1
rs4327090	17	43902541	17	43399058	44874453	A	G	0.2038	CRHR1	intronic	1.9705	0.1944	3.87E-24	2.1389	0.3398	3.28E-10	0.1162	0.0144	8.19E-16	1
rs3885074	17	43902738	17	43399058	44874453	A	C	0.2396	CRHR1	intronic	-1.9531	0.1798	1.74E-27	-2.2471	0.3215	3.07E-12	-0.1094	0.0132	9.86E-17	1
rs3885075	17	43902799	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9530	0.1798	1.76E-27	2.2470	0.3215	3.07E-12	0.1094	0.0132	9.83E-17	1
rs41280116	17	43902842	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9547	0.1802	1.99E-27	-2.2471	0.3215	3.07E-12	-0.1099	0.0132	1.04E-16	1
rs34283254	17	43902861	17	43399058	44874453	A	C	0.2396	CRHR1	exonic	-2.0702	0.2398	5.95E-18	-2.2471	0.3215	3.07E-12	-0.1099	0.0132	1.04E-16	1
rs1912151	17	43902944	17	43399058	44874453	T	C	0.2396	CRHR1	UTR3	-1.9530	0.1798	1.76E-27	-2.2468	0.3215	3.09E-12	-0.1095	0.0132	9.63E-17	1
rs1396862	17	43902997	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9535	0.1796	1.52E-27	-2.2468	0.3215	3.09E-12	-0.1095	0.0132	9.58E-17	1
rs41280118	17	43903089	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9530	0.1798	1.76E-27	-2.2469	0.3216	3.09E-12	-0.1096	0.0132	9.32E-17	1
rs62057146	17	43903106	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9528	0.1798	1.79E-27	2.2471	0.3216	3.07E-12	0.1096	0.0132	9.34E-17	1
rs62057147	17	43903298	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9505	0.18	2.32E-27	-2.2568	0.3216	2.51E-12	-0.1095	0.0132	1.01E-16	1
rs17763050	17	43903336	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9567	0.1802	1.81E-27	-2.2332	0.3223	4.66E-12	-0.1096	0.0132	9.21E-17	1
rs62057148	17	43903485	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	-1.9534	0.1798	1.72E-27	-2.2466	0.3216	3.11E-12	-0.1097	0.0132	9.14E-17	1
rs62057149	17	43903546	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	1.9535	0.1798	1.72E-27	2.2467	0.3216	3.10E-12	0.1097	0.0132	9.20E-17	1
rs62057150	17	43903548	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9535	0.1798	1.71E-27	-2.2467	0.3216	3.10E-12	-0.1097	0.0132	9.20E-17	1
rs62057151	17	43903842	17	43399058	44874453	T	C	0.2465	CRHR1	intronic	-1.9045	0.1786	1.52E-26	-2.1634	0.3175	1.04E-11	-0.1095	0.0132	1.09E-16	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs62057152	17	43904110	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	-2.0678	0.2391	5.16E-18	-2.2467	0.3216	3.10E-12	-0.1098	0.0132	8.81E-17	1
rs17689824	17	43904397	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9582	0.1799	1.36E-27	-2.2466	0.3216	3.11E-12	-0.1098	0.0132	8.92E-17	1
rs62057153	17	43904528	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9574	0.1798	1.32E-27	2.2466	0.3216	3.11E-12	0.1103	0.0132	6.21E-17	1
rs62057154	17	43904610	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9549	0.1799	1.61E-27	-2.2466	0.3216	3.11E-12	-0.1098	0.0132	8.64E-17	1
rs62057155	17	43904673	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9549	0.1799	1.62E-27	-2.2466	0.3216	3.11E-12	-0.1098	0.0132	8.67E-17	1
rs62057156	17	43904948	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	-1.9551	0.1799	1.61E-27	-2.2465	0.3216	3.13E-12	-0.1099	0.0132	8.53E-17	1
rs78872653	17	43905134	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9571	0.1802	1.82E-27	-2.2464	0.3216	3.13E-12	-0.1103	0.0133	9.02E-17	1
rs62057157	17	43905313	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	-1.9553	0.1799	1.60E-27	-2.2463	0.3216	3.14E-12	-0.1099	0.0132	8.29E-17	1
rs17763086	17	43905481	17	43399058	44874453	T	G	0.2396	CRHR1	intronic	1.9548	0.1799	1.69E-27	2.2467	0.3216	3.11E-12	0.1097	0.0132	9.74E-17	1
rs17425752	17	43906726	17	43399058	44874453	A	C	0.2386	CRHR1	intronic	1.9403	0.1804	5.63E-27	2.2560	0.3218	2.63E-12	0.1094	0.0133	1.58E-16	1
rs17689882	17	43906828	17	43399058	44874453	A	G	0.2386	CRHR1	intronic	-1.9325	0.1804	8.73E-27	-2.2580	0.3217	2.47E-12	-0.1089	0.0133	2.15E-16	1
rs62057158	17	43907143	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9554	0.18	1.68E-27	-2.2459	0.3216	3.18E-12	-0.1095	0.0132	1.07E-16	1
rs1876831	17	43907745	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9574	0.18	1.52E-27	-2.2456	0.3216	3.21E-12	-0.1096	0.0132	1.11E-16	1
rs16940665	17	43907896	17	43399058	44874453	T	C	0.2396	CRHR1	exonic	1.9556	0.18	1.67E-27	2.2456	0.3216	3.21E-12	0.1099	0.0132	8.89E-17	1
rs16940668	17	43907966	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9552	0.18	1.72E-27	-2.2456	0.3216	3.21E-12	-0.1098	0.0132	8.95E-17	1
rs16940671	17	43908151	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-2.0299	0.1873	2.28E-27	-2.2497	0.3221	3.17E-12	-0.1211	0.0147	1.94E-16	1
rs16940672	17	43908152	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-2.0290	0.1873	2.35E-27	-2.2493	0.3221	3.19E-12	-0.1211	0.0147	1.95E-16	1
rs55763795	17	43908773	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	-1.9556	0.18	1.68E-27	-2.2458	0.3216	3.18E-12	-0.1101	0.0132	9.21E-17	1
rs55865707	17	43908826	17	43399058	44874453	T	G	0.2396	CRHR1	intronic	1.9555	0.18	1.70E-27	2.2459	0.3216	3.18E-12	0.1101	0.0132	9.27E-17	1
rs62054760	17	43908989	17	43399058	44874453	T	C	0.2366	CRHR1	intronic	-1.9626	0.1805	1.54E-27	-2.2948	0.3235	1.46E-12	-0.1102	0.0133	9.71E-17	1
rs62054761	17	43909008	17	43399058	44874453	T	C	0.2366	CRHR1	intronic	-1.9631	0.1805	1.50E-27	-2.2939	0.3235	1.49E-12	-0.1101	0.0133	1.04E-16	1
rs62054762	17	43909022	17	43399058	44874453	T	G	0.2366	CRHR1	intronic	-1.9643	0.1805	1.41E-27	-2.2942	0.3236	1.48E-12	-0.1101	0.0133	1.03E-16	1
rs242951	17	43909412	17	43399058	44874453	T	C	0.4463	CRHR1	intronic	0.8272	0.1437	8.57E-09	1.1656	0.2731	2.01E-05	0.0555	0.0112	7.78E-07	1
rs17689918	17	43910088	17	43399058	44874453	A	G	0.2396	CRHR1	intronic	-1.9537	0.18	1.95E-27	-2.2486	0.3219	3.12E-12	-0.1102	0.0133	1.12E-16	1
rs17763199	17	43910183	17	43399058	44874453	A	G	0.2386	CRHR1	intronic	-1.9569	0.18	1.59E-27	-2.2471	0.3216	3.11E-12	-0.1101	0.0133	1.11E-16	1
rs62054763	17	43910262	17	43399058	44874453	C	G	0.2396	CRHR1	intronic	1.9570	0.18	1.59E-27	2.2458	0.3216	3.18E-12	0.1104	0.0133	1.05E-16	1
rs17689966	17	43910455	17	43399058	44874453	A	G	0.4443	CRHR1	intronic	0.8370	0.1444	6.76E-09	1.1752	0.2731	1.71E-05	0.0550	0.0112	9.84E-07	1
rs16940674	17	43910507	17	43399058	44874453	T	C	0.2396	CRHR1	exonic	-1.9567	0.1801	1.67E-27	-2.2458	0.3216	3.18E-12	-0.1104	0.0133	1.12E-16	1
rs16940676	17	43911036	17	43399058	44874453	A	G	0.2386	CRHR1	intronic	-1.9539	0.1802	2.17E-27	-2.2459	0.3216	3.18E-12	-0.1105	0.0133	1.12E-16	1
rs1876830	17	43911352	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9556	0.1802	1.96E-27	-2.2459	0.3216	3.18E-12	-0.1106	0.0133	1.11E-16	1
rs41457044	17	43911424	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9556	0.1802	1.97E-27	-2.2455	0.3216	3.21E-12	-0.1106	0.0133	1.14E-16	1
rs1876829	17	43911443	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9559	0.1802	1.97E-27	2.2459	0.3216	3.18E-12	0.1108	0.0134	1.11E-16	1
rs1876828	17	43911525	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9559	0.1802	1.98E-27	-2.2458	0.3216	3.18E-12	-0.1108	0.0134	1.15E-16	1
rs1876827	17	43911832	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	1.9560	0.1803	1.99E-27	2.2459	0.3216	3.18E-12	0.1110	0.0134	1.11E-16	1
rs16940677	17	43911898	17	43399058	44874453	T	C	0.2396	CRHR1	intronic	-1.9589	0.1802	1.60E-27	-2.2452	0.3217	3.25E-12	-0.1099	0.0135	3.50E-16	1
rs16940681	17	43912159	17	43399058	44874453	C	G	0.2396	CRHR1	exonic	-1.9561	0.1804	2.15E-27	-2.2545	0.3217	2.69E-12	-0.1100	0.0135	3.57E-16	1
rs28364021	17	43912282	17	43399058	44874453	T	C	0.2396	CRHR1	UTR3	-1.9565	0.1805	2.25E-27	-2.2459	0.3216	3.18E-12	-0.1101	0.0135	3.52E-16	1
rs2316765	17	43912454	17	43399058	44874453	T	C	0.2396	CRHR1	UTR3	1.9536	0.1811	4.04E-27	2.2474	0.3217	3.13E-12	0.1103	0.0135	3.41E-16	1
rs878886	17	43912490	17	43399058	44874453	C	G	0.2396	CRHR1	UTR3	1.9537	0.1811	4.01E-27	2.2476	0.3217	3.11E-12	0.1103	0.0135	3.51E-16	1
rs878887	17	43912582	17	43399058	44874453	T	C	0.2396	CRHR1	UTR3	-1.9532	0.1814	5.03E-27	-2.2475	0.3217	3.11E-12	-0.1104	0.0135	3.50E-16	1
rs878888	17	43912635	17	43399058	44874453	A	G	0.2396	CRHR1	UTR3	1.9457	0.1815	8.02E-27	2.2473	0.3217	3.13E-12	0.1102	0.0135	4.01E-16	1
rs4525537	17	43912723	17	43399058	44874453	T	C	0.2396	CRHR1	UTR3	1.9535	0.1814	4.97E-27	2.2468	0.3217	3.17E-12	0.1105	0.0135	3.42E-16	1
rs4640231	17	43912786	17	43399058	44874453	C	G	0.2396	CRHR1	UTR3	-1.9554	0.1816	5.00E-27	-2.2473	0.3217	3.13E-12	-0.1109	0.0136	2.93E-16	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs4482334	17	43912830	17	43399058	44874453	T	C	0.2396	CRHR1	UTR3	1.9529	0.1829	1.34E-26	2.2473	0.3217	3.13E-12	0.1107	0.0136	3.83E-16	1
rs56127111	17	43913315	17	43399058	44874453	T	C	0.2396	CRHR1	downstream	-1.9530	0.1829	1.33E-26	-2.2482	0.3217	3.05E-12	-0.1109	0.0136	3.99E-16	1
rs242948	17	43913544	17	43399058	44874453	T	G	0.4453	CRHR1	downstream	0.8361	0.1487	1.87E-08	1.1664	0.2735	2.03E-05	0.0570	0.0116	9.56E-07	1
rs75104593	17	43913557	17	43399058	44874453	T	G	0.2416	CRHR1	downstream	1.7913	0.1954	4.79E-20	2.2629	0.3251	3.71E-12	0.1204	0.0155	6.83E-15	1
rs74998289	17	43913558	17	43399058	44874453	T	G	0.2416	CRHR1	downstream	1.7887	0.1953	5.23E-20	2.2643	0.3250	3.59E-12	0.1192	0.0154	1.10E-14	1
rs10445362	17	43914554	17	43399058	44874453	A	C	0.2396	CRHR1	intergenic	-1.9800	0.1835	3.86E-27	-2.2496	0.3217	2.98E-12	-0.1123	0.0138	3.83E-16	1
rs10445363	17	43914558	17	43399058	44874453	A	G	0.2396	CRHR1	intergenic	-1.9513	0.1834	1.96E-26	-2.2496	0.3217	2.98E-12	-0.1104	0.0140	3.57E-15	1
rs62054802	17	43914598	17	43399058	44874453	C	G	0.2396	CRHR1	intergenic	-1.9802	0.1836	3.92E-27	-2.2495	0.3217	2.99E-12	-0.1124	0.0138	3.83E-16	1
rs62054803	17	43914728	17	43399058	44874453	T	G	0.2396	CRHR1	intergenic	-1.9804	0.1836	3.89E-27	-2.2493	0.3217	3.00E-12	-0.1113	0.0141	2.33E-15	1
rs62054804	17	43914809	17	43399058	44874453	T	C	0.2396	CRHR1	intergenic	-1.9817	0.1835	3.44E-27	-2.2503	0.3217	2.94E-12	-0.1113	0.0141	2.34E-15	1
rs62054805	17	43915054	17	43399058	44874453	A	G	0.2396	CRHR1	intergenic	1.9714	0.1844	1.09E-26	2.2495	0.3217	2.99E-12	0.1155	0.0147	3.95E-15	1
rs62054806	17	43915312	17	43399058	44874453	T	C	0.2396	CRHR1	intergenic	-2.1203	0.2484	1.37E-17	-2.2495	0.3217	2.99E-12	-0.1146	0.0145	3.06E-15	1
rs62054807	17	43915497	17	43399058	44874453	T	C	0.3201	CRHR1	intergenic	-1.4929	0.2229	2.12E-11	-1.5541	0.2950	1.43E-07	-0.0900	0.0127	1.28E-12	1
rs10445364	17	43916356	17	43399058	44874453	A	G	0.2396	CRHR1	intergenic	-2.1244	0.2489	1.40E-17	-2.2495	0.3217	2.99E-12	-0.1160	0.0147	2.61E-15	1
rs10445333	17	43916509	17	43399058	44874453	A	G	0.2396	CRHR1	intergenic	2.1188	0.249	1.76E-17	2.2493	0.3217	3.01E-12	0.1168	0.0149	5.15E-15	1
rs17690176	17	43916773	17	43399058	44874453	A	C	0.2406	CRHR1	intergenic	2.1120	0.2491	2.30E-17	2.2651	0.3216	2.08E-12	0.1169	0.0149	5.26E-15	1
rs78328427	17	43916932	17	43399058	44874453	A	G	0.2396	CRHR1	intergenic	-2.1132	0.2493	2.31E-17	-2.2554	0.3218	2.66E-12	-0.1171	0.0150	5.60E-15	1
rs77692262	17	43917086	17	43399058	44874453	A	G	0.2396	CRHR1	intergenic	2.1132	0.2493	2.31E-17	2.2496	0.3217	2.99E-12	0.1172	0.0150	5.63E-15	1
rs56023973	17	43917776	17	43399058	44874453	T	G	0.2396	MAPT-AS1	intergenic	-2.1382	0.2513	1.79E-17	-2.2492	0.3217	3.01E-12	-0.1174	0.0150	5.61E-15	1
rs17763515	17	43917818	17	43399058	44874453	A	G	0.2396	MAPT-AS1	intergenic	-2.1386	0.2513	1.76E-17	-2.2491	0.3217	3.01E-12	-0.1176	0.0151	5.57E-15	1
rs17763533	17	43918190	17	43399058	44874453	T	C	0.2396	MAPT-AS1	intergenic	2.1431	0.2513	1.49E-17	2.2493	0.3217	3.00E-12	0.1181	0.0151	5.16E-15	1
rs62054809	17	43918239	17	43399058	44874453	T	C	0.2396	MAPT-AS1	intergenic	-2.1397	0.2514	1.73E-17	-2.2479	0.3217	3.11E-12	-0.1180	0.0151	5.77E-15	1
rs112583797	17	43918418	17	43399058	44874453	A	G	0.2396	MAPT-AS1	intergenic	1.9877	0.1849	6.01E-27	2.2494	0.3217	3.00E-12	0.1181	0.0151	5.93E-15	1
rs74922289	17	43918524	17	43399058	44874453	A	G	0.2396	MAPT-AS1	intergenic	2.1383	0.2514	1.79E-17	2.2493	0.3217	3.00E-12	0.1182	0.0151	5.87E-15	1
rs56971664	17	43918613	17	43399058	44874453	T	C	0.2396	MAPT-AS1	intergenic	2.1319	0.251	2.01E-17	2.2508	0.3217	2.89E-12	0.1182	0.0151	6.10E-15	1
rs62054811	17	43918651	17	43399058	44874453	C	G	0.2396	MAPT-AS1	intergenic	2.1389	0.2514	1.77E-17	2.2492	0.3217	3.02E-12	0.1184	0.0152	5.77E-15	1
rs2106785	17	43919105	17	43399058	44874453	T	C	0.2386	MAPT-AS1	intergenic	-2.1223	0.2587	2.35E-16	-2.2404	0.3249	5.92E-12	-0.1215	0.0155	4.09E-15	1
rs56150806	17	43919301	17	43399058	44874453	T	C	0.2396	MAPT-AS1	intergenic	2.1358	0.2518	2.20E-17	2.2494	0.3217	3.00E-12	0.1189	0.0152	5.64E-15	1
rs17690314	17	43919884	17	43399058	44874453	T	G	0.2396	MAPT-AS1	intergenic	2.1359	0.2518	2.19E-17	2.2493	0.3217	3.00E-12	0.1190	0.0152	5.62E-15	1
rs56233672	17	43920300	17	43399058	44874453	T	C	0.2396	MAPT-AS1	downstream	2.0733	0.2562	5.87E-16	2.2492	0.3217	3.01E-12	0.1199	0.0153	4.93E-15	1
rs56354807	17	43920378	17	43399058	44874453	T	C	0.2396	MAPT-AS1	downstream	-2.1364	0.2518	2.18E-17	-2.2492	0.3217	3.01E-12	-0.1191	0.0152	5.82E-15	1
rs55718212	17	43920411	17	43399058	44874453	T	C	0.2396	MAPT-AS1	downstream	2.1362	0.2518	2.19E-17	2.2493	0.3217	3.01E-12	0.1191	0.0153	5.84E-15	1
rs17690326	17	43920974	17	43399058	44874453	T	C	0.2396	MAPT-AS1	downstream	2.1360	0.2519	2.27E-17	2.2492	0.3217	3.01E-12	0.1192	0.0153	5.90E-15	1
rs17763596	17	43921210	17	43399058	44874453	T	G	0.2396	MAPT-AS1	ncRNA_exonic	-2.1358	0.2519	2.29E-17	-2.2491	0.3217	3.01E-12	-0.1193	0.0153	5.56E-15	1
rs62054814	17	43921572	17	43399058	44874453	A	T	0.2396	MAPT-AS1	ncRNA_intronic	-2.1362	0.2519	2.27E-17	-2.2491	0.3217	3.01E-12	-0.1193	0.0153	5.93E-15	1
rs17763634	17	43921754	17	43399058	44874453	T	C	0.2396	MAPT-AS1	ncRNA_intronic	2.1360	0.2519	2.29E-17	2.2402	0.3218	3.70E-12	0.1193	0.0153	5.94E-15	1
rs62621252	17	43922942	17	43399058	44874453	T	C	0.2396	MAPT-AS1:SPPL2C	exonic	2.1351	0.252	2.37E-17	2.2216	0.3216	5.43E-12	0.1198	0.0153	5.92E-15	1
rs62054815	17	43923266	17	43399058	44874453	A	G	0.2396	MAPT-AS1:SPPL2C	exonic	-2.1345	0.252	2.44E-17	-2.2505	0.3217	2.90E-12	-0.1198	0.0154	5.93E-15	1
rs12185233	17	43923654	17	43399058	44874453	C	G	0.2396	MAPT-AS1:SPPL2C	exonic	-2.1341	0.252	2.49E-17	-2.2518	0.3218	2.87E-12	-0.1199	0.0154	5.92E-15	1
rs12185268	17	43923683	17	43399058	44874453	A	G	0.2396	MAPT-AS1:SPPL2C	exonic	2.1338	0.252	2.51E-17	2.2404	0.3215	3.54E-12	0.1200	0.0154	5.86E-15	1
rs12185235	17	43923703	17	43399058	44874453	T	C	0.2396	MAPT-AS1:SPPL2C	exonic	-2.1340	0.252	2.51E-17	-2.2647	0.3216	2.09E-12	-0.1201	0.0154	5.59E-15	1
rs11079725	17	43923934	17	43399058	44874453	T	C	0.2396	MAPT-AS1:SPPL2C	exonic	2.1341	0.252	2.50E-17	2.2473	0.3215	3.04E-12	0.1200	0.0154	5.90E-15	1
rs12373123	17	43924073	17	43399058	44874453	T	C	0.2396	MAPT-AS1:SPPL2C	exonic	2.1328	0.252	2.62E-17	2.2475	0.3215	3.03E-12	0.1201	0.0154	5.84E-15	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs12373139	17	43924130	17	43399058	44874453	A	G	0.2396	MAPT-AS1:SPPL2C	exonic	-2.1328	0.252	2.63E-17	-2.2477	0.3215	3.01E-12	-0.1201	0.0154	5.88E-15	1
rs12373142	17	43924200	17	43399058	44874453	C	G	0.2396	MAPT-AS1:SPPL2C	exonic	2.0535	0.2564	1.15E-15	2.2616	0.3236	3.04E-12	0.1202	0.0155	1.02E-14	1
rs12373124	17	43924219	17	43399058	44874453	T	C	0.2396	MAPT-AS1:SPPL2C	exonic	2.0531	0.2564	1.17E-15	2.2621	0.3237	3.06E-12	0.1208	0.0155	7.72E-15	1
rs12373140	17	43924231	17	43399058	44874453	A	G	0.2396	MAPT-AS1:SPPL2C	exonic	-2.0530	0.2564	1.17E-15	-2.2619	0.3237	3.07E-12	-0.1209	0.0155	7.71E-15	1
rs12373168	17	43924337	17	43399058	44874453	A	C	0.2425	MAPT-AS1:SPPL2C	ncRNA_intronic	2.1048	0.2501	3.85E-17	2.2035	0.3206	6.92E-12	0.1216	0.0157	8.79E-15	1
rs17690661	17	43924521	17	43399058	44874453	A	G	0.2396	MAPT-AS1	ncRNA_intronic	-2.0333	0.2611	6.85E-15	-2.2472	0.3215	3.04E-12	-0.1213	0.0156	7.57E-15	1
rs55943825	17	43924776	17	43399058	44874453	T	C	0.2396	MAPT-AS1	ncRNA_intronic	-2.0267	0.2607	7.55E-15	-2.2474	0.3215	3.03E-12	-0.1218	0.0156	6.05E-15	1
rs17690679	17	43924803	17	43399058	44874453	A	G	0.2396	MAPT-AS1	ncRNA_intronic	2.0267	0.2607	7.55E-15	2.2474	0.3215	3.03E-12	0.1220	0.0156	5.99E-15	1
rs17690703	17	43925297	17	43399058	44874453	T	C	0.2763	MAPT-AS1	ncRNA_intronic	-1.8035	0.2474	3.08E-13	-1.8754	0.3059	9.27E-10	-0.1012	0.0154	4.93E-11	1
rs17769490	17	43925605	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	-2.0004	0.2603	1.54E-14	-2.2321	0.3205	3.64E-12	-0.1219	0.0157	7.04E-15	1
rs77063768	17	43925729	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	2.0212	0.2604	8.31E-15	2.2321	0.3205	3.65E-12	0.1218	0.0157	7.94E-15	1
rs62054817	17	43925966	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	-2.0225	0.2604	8.05E-15	-2.2319	0.3205	3.66E-12	-0.1220	0.0157	8.48E-15	1
rs62054818	17	43926056	17	43399058	44874453	A	C	0.2406	MAPT-AS1	ncRNA_intronic	2.0204	0.2604	8.60E-15	2.2315	0.3205	3.69E-12	0.1221	0.0157	8.53E-15	1
rs62054819	17	43926149	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	2.0424	0.2611	5.22E-15	2.2314	0.3205	3.70E-12	0.1220	0.0158	1.33E-14	1
rs62054820	17	43926755	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	2.0209	0.2605	8.56E-15	2.2320	0.3205	3.67E-12	0.1223	0.0158	8.57E-15	1
rs56113217	17	43926948	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	2.0209	0.2605	8.60E-15	2.2196	0.3209	5.05E-12	0.1225	0.0158	8.39E-15	1
rs56269136	17	43926992	17	43399058	44874453	T	C	0.2406	MAPT-AS1	ncRNA_intronic	-2.0208	0.2605	8.65E-15	-2.2305	0.3208	3.94E-12	-0.1226	0.0158	8.56E-15	1
rs56385754	17	43927255	17	43399058	44874453	T	G	0.2406	MAPT-AS1	ncRNA_intronic	-2.0207	0.2605	8.65E-15	-2.2360	0.3205	3.35E-12	-0.1227	0.0158	8.56E-15	1
rs17769552	17	43927290	17	43399058	44874453	A	G	0.2326	MAPT-AS1	ncRNA_intronic	-1.7713	0.2736	9.48E-11	-2.2569	0.3234	3.28E-12	-0.1250	0.0161	9.78E-15	1
rs62054822	17	43927708	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	2.0225	0.26	7.26E-15	2.2241	0.3201	4.09E-12	0.1230	0.0159	8.84E-15	1
rs885639	17	43928614	17	43399058	44874453	T	G	0.2406	MAPT-AS1	ncRNA_intronic	2.0210	0.2594	6.73E-15	2.2414	0.3202	2.84E-12	0.1231	0.0159	1.03E-14	1
rs62054823	17	43929029	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	2.0119	0.2607	1.20E-14	2.2246	0.3210	4.64E-12	0.1240	0.0159	7.08E-15	1
rs62054824	17	43929992	17	43399058	44874453	T	C	0.2396	MAPT-AS1	ncRNA_intronic	-2.0265	0.2615	9.16E-15	-2.2349	0.3214	3.94E-12	-0.1252	0.0162	1.26E-14	1
rs62054825	17	43930033	17	43399058	44874453	A	G	0.2406	MAPT-AS1	ncRNA_intronic	-2.0273	0.2614	8.82E-15	-2.2339	0.3214	4.02E-12	-0.1250	0.0162	1.40E-14	1
rs79589869	17	43930238	17	43399058	44874453	A	C	0.2396	MAPT-AS1	ncRNA_intronic	-2.0275	0.2615	9.04E-15	-2.2374	0.3216	3.84E-12	-0.1253	0.0163	1.27E-14	1
rs2316769	17	43930798	17	43399058	44874453	A	G	0.2396	MAPT-AS1	ncRNA_intronic	1.7964	0.2707	3.23E-11	2.2301	0.3214	4.34E-12	0.1299	0.0167	7.84E-15	1
rs2873268	17	43930955	17	43399058	44874453	A	G	0.2396	MAPT-AS1	ncRNA_intronic	-1.7955	0.2708	3.32E-11	-2.2447	0.3216	3.25E-12	-0.1300	0.0167	8.36E-15	1
rs113856644	17	43932277	17	43399058	44874453	A	G	0.2396	MAPT-AS1	ncRNA_intronic	-1.7630	0.1949	1.49E-19	-2.2260	0.3214	4.73E-12	NA	NA	NA	NA
rs76563578	17	43933879	17	43399058	44874453	C	G	0.2396	MAPT-AS1	ncRNA_intronic	1.7496	0.1941	1.97E-19	2.2031	0.3212	7.58E-12	NA	NA	NA	NA
rs111962225	17	43934016	17	43399058	44874453	C	G	0.2396	MAPT-AS1	ncRNA_intronic	-1.7490	0.1941	2.02E-19	-2.2008	0.3212	7.99E-12	NA	NA	NA	NA
rs62054835	17	43934672	17	43399058	44874453	A	C	0.2396	MAPT-AS1	ncRNA_intronic	1.7514	0.1941	1.83E-19	2.1999	0.3211	8.09E-12	NA	NA	NA	NA
rs113414067	17	43955093	17	43399058	44874453	T	C	0.2396	MAPT-AS1	ncRNA_intronic	1.7504	0.1939	1.76E-19	2.2023	0.3212	7.75E-12	NA	NA	NA	NA
rs62056785	17	43975263	17	43399058	44874453	T	C	0.2396	MAPT	intronic	1.7524	0.1939	1.60E-19	2.2029	0.3212	7.67E-12	NA	NA	NA	NA
rs62056786	17	43975285	17	43399058	44874453	T	C	0.2396	MAPT	intronic	1.7469	0.1939	2.04E-19	2.2029	0.3212	7.67E-12	NA	NA	NA	NA
rs62056789	17	43975415	17	43399058	44874453	A	C	0.2396	MAPT	intronic	1.7582	0.1945	1.56E-19	2.2030	0.3212	7.66E-12	NA	NA	NA	NA
rs62056790	17	43975417	17	43399058	44874453	A	G	0.2396	MAPT	intronic	-1.7581	0.1945	1.57E-19	-2.2030	0.3212	7.66E-12	NA	NA	NA	NA
rs113589236	17	43981795	17	43399058	44874453	A	G	0.2396	MAPT	intronic	-1.7176	0.1951	1.33E-18	-2.2037	0.3212	7.56E-12	NA	NA	NA	NA
rs113029914	17	43981831	17	43399058	44874453	A	T	0.2396	MAPT	intronic	1.7243	0.1952	9.99E-19	2.2037	0.3212	7.56E-12	NA	NA	NA	NA
rs112275277	17	43981958	17	43399058	44874453	T	C	0.2396	MAPT	intronic	-1.7104	0.1944	1.38E-18	-2.2030	0.3212	7.66E-12	NA	NA	NA	NA
rs62056851	17	43992806	17	43399058	44874453	A	G	0.2396	MAPT	intronic	1.7104	0.1944	1.37E-18	2.1974	0.3214	8.83E-12	NA	NA	NA	NA
rs9899833	17	43992943	17	43399058	44874453	A	G	0.3608	MAPT	intronic	-1.0198	0.1746	5.18E-09	-1.7456	0.2850	9.56E-10	NA	NA	NA	NA
rs111541901	17	43994358	17	43399058	44874453	T	C	0.2396	MAPT	intronic	-1.7080	0.1948	1.79E-18	-2.1815	0.3218	1.32E-11	NA	NA	NA	NA
rs112647192	17	43994623	17	43399058	44874453	A	G	0.2396	MAPT	intronic	-1.7092	0.1944	1.45E-18	-2.1969	0.3214	8.94E-12	NA	NA	NA	NA

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs62059005	17	44004472	17	43399058	44874453	A	G	0.2396	MAPT	intronic	1.7098	0.1944	1.45E-18	2.2034	0.3212	7.60E-12	NA	NA	NA	NA
rs113796169	17	44005254	17	43399058	44874453	A	T	0.2406	MAPT	intronic	-1.7089	0.1945	1.58E-18	-2.2013	0.3213	7.99E-12	NA	NA	NA	NA
rs112454267	17	44005329	17	43399058	44874453	A	G	0.2406	MAPT	intronic	-1.7154	0.1944	1.12E-18	-2.2013	0.3213	7.99E-12	NA	NA	NA	NA
rs78026984	17	44025592	17	43399058	44874453	C	G	0.2396	MAPT	intronic	-1.7373	0.1956	6.53E-19	-2.2161	0.3214	5.90E-12	NA	NA	NA	NA
rs113520245	17	44033132	17	43399058	44874453	T	C	0.2396	MAPT	intronic	-1.7524	0.1973	6.50E-19	-2.2325	0.3270	9.50E-12	NA	NA	NA	NA
rs62063271	17	44036047	17	43399058	44874453	A	G	0.2396	MAPT	intronic	-1.7575	0.1955	2.44E-19	-2.2245	0.3215	4.99E-12	NA	NA	NA	NA
rs62641967	17	44047216	17	43399058	44874453	T	G	0.2406	MAPT	intronic	1.7517	0.1953	2.94E-19	2.2173	0.3215	5.85E-12	NA	NA	NA	NA
rs117124984	17	44051588	17	43399058	44874453	C	G	0.2406	MAPT	UTR5	1.7903	0.1991	2.41E-19	2.2264	0.3269	1.06E-11	NA	NA	NA	NA
rs118087478	17	44051589	17	43399058	44874453	T	G	0.2406	MAPT	UTR5	1.7955	0.1991	1.88E-19	2.2265	0.3269	1.06E-11	NA	NA	NA	NA
rs112385572	17	44066172	17	43399058	44874453	A	G	0.2406	MAPT	intronic	1.7487	0.1952	3.26E-19	2.2175	0.3214	5.72E-12	NA	NA	NA	NA
rs112572874	17	44072984	17	43399058	44874453	A	G	0.2406	MAPT	intronic	1.7292	0.1949	7.27E-19	2.1708	0.3213	1.54E-11	NA	NA	NA	NA
rs62062278	17	44093860	17	43399058	44874453	A	G	0.2406	MAPT	intronic	1.7451	0.1955	4.31E-19	2.2178	0.3214	5.68E-12	NA	NA	NA	NA
rs112578465	17	44125066	17	43399058	44874453	T	C	0.2406	KANSL1	intronic	-1.7455	0.1953	4.04E-19	-2.2174	0.3214	5.73E-12	NA	NA	NA	NA
rs112746008	17	44126650	17	43399058	44874453	T	C	0.2406	KANSL1	intronic	-1.7655	0.1971	3.34E-19	-2.2122	0.3214	6.45E-12	NA	NA	NA	NA
rs112333322	17	44126673	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	1.7418	0.1968	8.74E-19	2.2483	0.3230	3.73E-12	NA	NA	NA	NA
rs111327992	17	44126691	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	-1.7346	0.1953	6.47E-19	-2.1932	0.3213	9.59E-12	NA	NA	NA	NA
rs113434679	17	44126765	17	43399058	44874453	A	C	0.2028	KANSL1	intronic	-1.6822	0.2087	7.64E-16	-2.0696	0.3387	1.05E-09	NA	NA	NA	NA
rs17575507	17	44134095	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	1.7394	0.1953	5.29E-19	2.2117	0.3214	6.52E-12	NA	NA	NA	NA
rs111372048	17	44136577	17	43399058	44874453	A	C	0.2406	KANSL1	intronic	1.7328	0.1953	7.26E-19	2.2035	0.3215	7.85E-12	NA	NA	NA	NA
rs112197756	17	44154105	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	1.7352	0.1954	6.58E-19	2.2178	0.3214	5.68E-12	NA	NA	NA	NA
rs111913701	17	44159631	17	43399058	44874453	T	G	0.2406	KANSL1	intronic	1.7346	0.1954	6.81E-19	2.2177	0.3214	5.69E-12	NA	NA	NA	NA
rs111519055	17	44159672	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	1.7347	0.1954	6.80E-19	2.2177	0.3214	5.69E-12	NA	NA	NA	NA
rs113788190	17	44161302	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	1.7346	0.1954	6.83E-19	2.2177	0.3214	5.70E-12	NA	NA	NA	NA
rs112364920	17	44161360	17	43399058	44874453	A	T	0.2396	KANSL1	intronic	1.7346	0.1954	6.83E-19	2.2177	0.3214	5.70E-12	NA	NA	NA	NA
rs80028338	17	44161470	17	43399058	44874453	A	C	0.2406	KANSL1	intronic	1.7764	0.2035	2.59E-18	2.3703	0.3421	4.65E-12	NA	NA	NA	NA
rs111970616	17	44169581	17	43399058	44874453	T	C	0.2406	KANSL1	intronic	1.7816	0.1966	1.26E-19	2.2166	0.3214	5.85E-12	NA	NA	NA	NA
rs112596352	17	44170238	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	-1.7259	0.1955	1.05E-18	-2.1992	0.3213	8.36E-12	NA	NA	NA	NA
rs111676341	17	44183403	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	1.7642	0.1965	2.80E-19	2.1985	0.3214	8.62E-12	NA	NA	NA	NA
rs112560196	17	44200078	17	43399058	44874453	A	T	0.2406	KANSL1	intronic	1.7445	0.1962	6.00E-19	2.1970	0.3215	9.01E-12	NA	NA	NA	NA
rs112073200	17	44201791	17	43399058	44874453	C	G	0.2406	KANSL1	intronic	-1.7299	0.1967	1.45E-18	-2.1887	0.3216	1.09E-11	NA	NA	NA	NA
rs55669501	17	44202564	17	43399058	44874453	A	G	0.2406	KANSL1	intronic	-1.7436	0.1965	7.02E-19	-2.1888	0.3215	1.08E-11	NA	NA	NA	NA
rs55686102	17	44202608	17	43399058	44874453	T	C	0.2406	KANSL1	intronic	-1.7436	0.1965	7.03E-19	-2.1888	0.3215	1.09E-11	NA	NA	NA	NA
NA	17	44699851	17	43399058	44874453	A	G	0.2197	NSF	intronic	-2.5768	0.3085	6.72E-17	-2.2087	0.3374	6.35E-11	-0.1189	0.0195	1.19E-09	1
rs117300236	17	44753350	17	43399058	44874453	A	G	0.2843	NSF	intronic	-1.9285	0.1977	1.76E-22	-1.7289	0.3222	8.36E-08	NA	NA	NA	NA
rs199461	17	44762589	17	43399058	44874453	A	G	0.2555	NSF	intronic	-1.7751	0.2101	2.94E-17	-1.9600	0.3171	6.80E-10	-0.0900	0.0129	2.91E-12	1
rs199460	17	44764775	17	43399058	44874453	A	C	0.2187	NSF	intronic	2.0439	0.2516	4.50E-16	2.1775	0.3491	4.73E-10	0.1045	0.0150	3.72E-12	1
rs199441	17	44773783	17	43399058	44874453	A	G	0.2306	NSF	intronic	-2.0726	0.2125	1.79E-22	-2.1373	0.3259	5.88E-11	-0.1072	0.0130	1.30E-16	1
rs199437	17	44786336	17	43399058	44874453	A	T	0.2575	NSF	intronic	-1.6670	0.1605	2.78E-25	-1.9276	0.3164	1.19E-09	-0.0844	0.0120	1.74E-12	1
rs1378358	17	44787312	17	43399058	44874453	T	C	0.2247	NSF	intronic	-2.0049	0.171	9.55E-32	-2.2033	0.3276	1.91E-11	-0.1091	0.0130	4.12E-17	1
rs538628	17	44787313	17	43399058	44874453	C	G	0.2247	NSF	intronic	-2.0044	0.171	9.74E-32	-2.1925	0.3276	2.38E-11	-0.1089	0.0130	4.16E-17	1
rs183211	17	44788310	17	43399058	44874453	A	G	0.2584	NSF	intronic	-1.6535	0.16	4.77E-25	-1.9271	0.3164	1.19E-09	-0.0840	0.0119	1.69E-12	1
rs199436	17	44789285	17	43399058	44874453	A	G	0.2575	NSF	intronic	1.6504	0.1599	5.47E-25	1.9271	0.3164	1.19E-09	0.0839	0.0119	1.62E-12	1
rs169201	17	44790203	17	43399058	44874453	A	G	0.2247	NSF	intronic	1.9379	0.1672	4.66E-31	2.2175	0.3276	1.41E-11	0.1050	0.0125	4.53E-17	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs199438	17	44791643	17	43399058	44874453	A	G	0.2575	NSF	intronic	-1.6479	0.1597	5.83E-25	-1.9273	0.3164	1.19E-09	-0.0839	0.0118	1.43E-12	1
rs17692129	17	44793283	17	43399058	44874453	T	C	0.34	NSF	intronic	1.0218	0.1596	1.53E-10	1.1869	0.2842	3.00E-05	0.0573	0.0125	4.32E-06	1
rs199439	17	44793503	17	43399058	44874453	A	G	0.2247	NSF	intronic	1.9309	0.1671	6.72E-31	2.1957	0.3276	2.22E-11	0.1048	0.0125	3.94E-17	1
rs142167	17	44795234	17	43399058	44874453	A	G	0.2575	NSF	intronic	1.6441	0.1596	6.84E-25	1.9241	0.3164	1.27E-09	0.0837	0.0118	1.23E-12	1
rs199457	17	44795469	17	43399058	44874453	T	C	0.2247	NSF	intronic	-1.9316	0.167	6.29E-31	-2.2140	0.3276	1.52E-11	-0.1046	0.0124	3.84E-17	1
rs199456	17	44797919	17	43399058	44874453	T	C	0.2247	NSF	intronic	-1.9254	0.167	9.74E-31	-2.2058	0.3277	1.84E-11	-0.1045	0.0124	3.87E-17	1
rs199455	17	44799216	17	43399058	44874453	T	C	0.2614	NSF:RPS7P11	ncRNA_exonic	1.6216	0.1593	2.40E-24	1.8856	0.3159	2.53E-09	0.0831	0.0118	1.61E-12	1
rs7224296	17	44800046	17	43399058	44874453	A	G	0.3022	NSF	intronic	1.4177	0.1545	4.53E-20	1.7800	0.3021	4.02E-09	0.0768	0.0115	2.66E-11	1
rs199454	17	44800110	17	43399058	44874453	A	G	0.2594	NSF	intronic	1.6287	0.1595	1.71E-24	1.8933	0.3158	2.15E-09	0.0830	0.0118	1.62E-12	1
rs199453	17	44800946	17	43399058	44874453	T	C	0.2584	NSF	intronic	-1.6439	0.1596	7.17E-25	-1.9237	0.3166	1.30E-09	-0.0831	0.0118	1.60E-12	1
rs199452	17	44801340	17	43399058	44874453	T	C	0.2565	NSF	intronic	-1.6403	0.1597	9.68E-25	-1.9361	0.3169	1.05E-09	-0.0836	0.0118	1.17E-12	1
rs199451	17	44801784	17	43399058	44874453	A	G	0.2227	NSF	intronic	-1.9281	0.1671	8.17E-31	-2.2194	0.3277	1.37E-11	-0.1052	0.0124	2.18E-17	1
rs35937770	17	44808360	17	43399058	44874453	A	G	0.339	NSF	intronic	0.9826	0.1592	6.70E-10	1.2214	0.2858	1.96E-05	0.0602	0.0125	1.57E-06	1
rs199449	17	44808902	17	43399058	44874453	A	G	0.2555	NSF	intronic	-1.6343	0.1599	1.57E-24	-1.9408	0.3168	9.56E-10	-0.0839	0.0118	1.06E-12	1
rs199448	17	44809001	17	43399058	44874453	A	G	0.2227	NSF	intronic	1.9246	0.1672	1.15E-30	2.2277	0.3279	1.19E-11	0.1054	0.0124	2.05E-17	1
rs199447	17	44812188	17	43399058	44874453	T	C	0.2227	NSF	intronic	-1.9220	0.1672	1.39E-30	-2.2267	0.3279	1.22E-11	-0.1054	0.0124	2.01E-17	1
rs199446	17	44813169	17	43399058	44874453	A	G	0.2575	NSF	intronic	1.6239	0.1597	2.81E-24	1.9073	0.3160	1.68E-09	0.0836	0.0118	1.29E-12	1
rs199445	17	44817408	17	43399058	44874453	T	C	0.2227	NSF	intronic	-1.9133	0.1672	2.64E-30	-2.2057	0.3279	1.88E-11	-0.1056	0.0124	1.69E-17	1
rs199444	17	44818276	17	43399058	44874453	T	C	0.2555	NSF	intronic	1.6317	0.1601	2.14E-24	1.9367	0.3168	1.03E-09	0.0849	0.0118	6.01E-13	1
rs199443	17	44819565	17	43399058	44874453	T	C	0.2227	NSF	intronic	-1.9144	0.1673	2.49E-30	-2.2029	0.3279	1.99E-11	-0.1059	0.0124	1.37E-17	1
rs199442	17	44820122	17	43399058	44874453	A	G	0.2555	NSF	intronic	-1.6277	0.1601	2.88E-24	-1.9347	0.3168	1.07E-09	-0.0853	0.0118	4.94E-13	1
rs199536	17	44820425	17	43399058	44874453	T	C	0.2575	NSF	intronic	-1.6194	0.1599	4.26E-24	-1.9033	0.3160	1.80E-09	-0.0847	0.0118	6.50E-13	1
rs199535	17	44822662	17	43399058	44874453	A	G	0.2227	NSF	intronic	1.9174	0.1673	2.03E-30	2.2015	0.3278	2.03E-11	0.1063	0.0124	9.80E-18	1
rs199534	17	44824213	17	43399058	44874453	T	G	0.2227	NSF	intronic	1.9156	0.1672	2.25E-30	2.2212	0.3278	1.35E-11	0.1059	0.0124	1.32E-17	1
rs9896243	17	44826056	17	43399058	44874453	C	G	0.2256	NSF	intronic	1.9152	0.1672	2.23E-30	2.1692	0.3272	3.66E-11	0.1061	0.0124	1.20E-17	1
rs199533	17	44828931	17	43399058	44874453	A	G	0.2227	NSF	exonic	-1.9104	0.1671	2.77E-30	-2.1675	0.3264	3.41E-11	-0.1063	0.0124	9.98E-18	1
rs199531	17	44830414	17	43399058	44874453	T	C	0.2565	NSF	intronic	1.6310	0.1601	2.20E-24	1.8917	0.3152	2.06E-09	0.0863	0.0118	2.94E-13	1
rs9912530	17	44836302	17	43399058	44874453	T	C	0.3002	NSF	intergenic	-1.4129	0.1555	1.06E-19	-1.7485	0.3013	6.80E-09	-0.0809	0.0116	3.69E-12	1
rs199530	17	44836653	17	43399058	44874453	A	G	0.2604	NSF	intergenic	1.6122	0.16	7.19E-24	1.8552	0.3148	4.00E-09	0.0856	0.0118	4.86E-13	1
rs199529	17	44837217	17	43399058	44874453	A	C	0.2425	NSF	intergenic	1.8033	0.1642	4.68E-28	2.0280	0.3187	2.11E-10	0.0982	0.0122	9.45E-16	1
rs199528	17	44843136	17	43399058	44874453	T	C	0.2207	WNT3	intronic	-1.9060	0.1681	8.55E-30	-2.1992	0.3263	1.72E-11	-0.1076	0.0125	8.36E-18	1
rs199527	17	44843667	17	43399058	44874453	A	G	0.2575	WNT3	intronic	1.6287	0.1616	7.02E-24	1.8801	0.3145	2.40E-09	0.0871	0.0120	3.58E-13	1
rs199526	17	44847707	17	43399058	44874453	C	G	0.2366	WNT3	intronic	-1.7499	0.1656	4.09E-26	-2.0385	0.3212	2.37E-10	-0.0971	0.0123	2.85E-15	1
rs199525	17	44847834	17	43399058	44874453	T	G	0.2207	WNT3	intronic	1.9041	0.168	8.89E-30	2.2045	0.3260	1.48E-11	0.1074	0.0125	9.21E-18	1
rs3809857	17	44848314	17	43399058	44874453	T	G	0.331	WNT3	intronic	1.0365	0.1653	3.57E-10	1.1860	0.2865	3.52E-05	0.0620	0.0130	1.95E-06	1
rs199524	17	44848438	17	43399058	44874453	T	G	0.2575	WNT3	intronic	1.6151	0.1614	1.38E-23	1.8934	0.3151	1.97E-09	0.0869	0.0119	3.38E-13	1
rs199523	17	44848517	17	43399058	44874453	A	C	0.2575	WNT3	intronic	1.6005	0.1617	4.21E-23	1.8950	0.3151	1.91E-09	0.0864	0.0120	7.11E-13	1
rs199521	17	44853456	17	43399058	44874453	C	G	0.2555	WNT3	intronic	1.6389	0.1616	3.64E-24	1.8990	0.3152	1.80E-09	0.0856	0.0119	6.87E-13	1
rs199520	17	44853872	17	43399058	44874453	A	G	0.2575	WNT3	intronic	1.6391	0.1616	3.50E-24	1.9083	0.3152	1.50E-09	0.0856	0.0119	6.72E-13	1
rs199519	17	44853924	17	43399058	44874453	A	G	0.2575	WNT3	intronic	1.6447	0.1615	2.34E-24	1.8957	0.3150	1.86E-09	0.0856	0.0119	6.90E-13	1
rs199518	17	44854580	17	43399058	44874453	A	C	0.2575	WNT3	intronic	-1.6550	0.1632	3.68E-24	-1.8810	0.3158	2.73E-09	-0.0896	0.0122	2.30E-13	1
rs199517	17	44854587	17	43399058	44874453	A	G	0.2575	WNT3	intronic	-1.6530	0.1631	3.87E-24	-1.8807	0.3157	2.71E-09	-0.0891	0.0122	2.85E-13	1
rs199516	17	44856485	17	43399058	44874453	T	C	0.2207	WNT3	intronic	1.9081	0.1678	5.74E-30	2.2211	0.3249	8.96E-12	0.1053	0.0125	2.83E-17	1

rsID	chr	pos (hg19)	Genomic Locus	Genomic Locus start	Genomic Locus end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs199515	17	44856641	17	43399058	44874453	C	G	0.2177	WNT3	intronic	1.9060	0.1678	6.78E-30	2.2324	0.3249	7.00E-12	0.1049	0.0125	3.91E-17	1
rs199514	17	44856881	17	43399058	44874453	A	G	0.2187	WNT3	intronic	1.9126	0.1677	3.99E-30	2.2162	0.3249	9.91E-12	0.1052	0.0124	2.71E-17	1
rs199513	17	44856932	17	43399058	44874453	A	G	0.2167	WNT3	intronic	-1.9148	0.1678	3.75E-30	-2.2163	0.3249	9.89E-12	-0.1050	0.0125	3.62E-17	1
rs199512	17	44857352	17	43399058	44874453	T	C	0.2197	WNT3	intronic	-1.9163	0.1679	3.47E-30	-2.2105	0.3250	1.12E-11	-0.1052	0.0124	2.78E-17	1
NA	17	44857929	17	43399058	44874453	A	C	0.2197	WNT3	intronic	-2.0733	0.2367	1.94E-18	-2.2053	0.3250	1.27E-11	-0.1062	0.0126	3.19E-17	1
rs199509	17	44858728	17	43399058	44874453	A	G	0.2197	WNT3	intronic	1.9140	0.1678	4.02E-30	2.2229	0.3250	8.67E-12	0.1052	0.0124	2.78E-17	1
rs199508	17	44858838	17	43399058	44874453	C	G	0.2565	WNT3	intronic	-1.6831	0.1624	3.58E-25	-1.9043	0.3153	1.64E-09	-0.0870	0.0119	3.05E-13	1
rs199507	17	44858855	17	43399058	44874453	A	G	0.2197	WNT3	intronic	-1.9149	0.1679	3.90E-30	-2.2231	0.3250	8.64E-12	-0.1052	0.0124	2.78E-17	1
rs199506	17	44859031	17	43399058	44874453	A	G	0.2197	WNT3	intronic	-1.9138	0.168	4.69E-30	-2.2323	0.3250	7.13E-12	-0.1052	0.0125	3.37E-17	1
rs415430	17	44859144	17	43399058	44874453	T	C	0.2167	WNT3	intronic	1.9158	0.168	4.11E-30	2.2239	0.3250	8.55E-12	0.1055	0.0125	2.83E-17	1
rs430685	17	44859148	17	43399058	44874453	T	C	0.2167	WNT3	intronic	-1.9159	0.168	4.07E-30	-2.2239	0.3250	8.54E-12	-0.1055	0.0125	2.92E-17	1
rs199505	17	44859410	17	43399058	44874453	A	G	0.2177	WNT3	intronic	-1.9149	0.1681	4.67E-30	-2.2317	0.3252	7.47E-12	-0.1056	0.0125	2.78E-17	1
rs70602	17	44859715	17	43399058	44874453	T	C	0.2177	WNT3	intronic	-1.9146	0.1682	5.15E-30	-2.2289	0.3254	8.07E-12	-0.1056	0.0125	2.70E-17	1
rs70600	17	44860021	17	43399058	44874453	T	C	0.2177	WNT3	intronic	-1.9256	0.1683	2.60E-30	-2.2457	0.3262	6.35E-12	-0.1057	0.0125	2.67E-17	1
rs199504	17	44861003	17	43399058	44874453	T	C	0.2207	WNT3	intronic	1.9200	0.1683	3.80E-30	2.2057	0.3251	1.28E-11	0.1055	0.0125	3.35E-17	1
NA	17	44862162	17	43399058	44874453	A	G	0.2197	WNT3	intronic	-2.0964	0.2437	7.78E-18	-2.2480	0.3267	6.51E-12	-0.1097	0.0128	9.97E-18	1
rs199502	17	44862347	17	43399058	44874453	A	G	0.2326	WNT3	intronic	-1.8352	0.1686	1.40E-27	-2.1448	0.3277	6.45E-11	-0.0949	0.0124	1.70E-14	1
rs199501	17	44862613	17	43399058	44874453	A	G	0.2525	WNT3	intronic	-1.7066	0.1635	1.72E-25	-2.0012	0.3162	2.65E-10	-0.0894	0.0121	1.27E-13	1
rs916888	17	44863133	17	43399058	44874453	T	C	0.2654	WNT3	intronic	1.6437	0.1673	8.71E-23	2.1307	0.3099	6.83E-12	0.1001	0.0124	6.70E-16	1
rs199500	17	44863413	17	43399058	44874453	T	C	0.2734	WNT3	intronic	-1.5514	0.1684	3.22E-20	-1.9120	0.3063	4.57E-10	-0.1018	0.0127	1.37E-15	1
rs2074404	17	44865439	17	43399058	44874453	T	G	0.2664	WNT3	intronic	1.4180	0.1669	1.96E-17	1.8595	0.3267	1.31E-08	0.0843	0.0120	2.53E-12	1
rs199499	17	44865498	17	43399058	44874453	T	C	0.2078	WNT3	intronic	-1.8702	0.182	8.85E-25	-2.2314	0.3559	3.87E-10	-0.1123	0.0135	7.47E-17	1
rs199498	17	44865603	17	43399058	44874453	T	C	0.2247	WNT3	intronic	1.7129	0.1774	4.63E-22	2.0385	0.3420	2.64E-09	0.0981	0.0130	4.01E-14	1
rs199497	17	44866602	17	43399058	44874453	T	C	0.1809	WNT3	intronic	1.3391	0.2139	3.82E-10	1.1787	0.3699	1.45E-03	NA	NA	NA	NA
rs1563304	17	44874453	17	43399058	44874453	T	C	0.1829	WNT3	intronic	-1.5441	0.2783	2.90E-08	-1.0230	0.3474	3.25E-03	-0.0799	0.0191	2.78E-05	1
rs35895680	17	47060322	18	47060322	47145848	A	C	0.2992	RP11-501C14.5	intergenic	0.8719	0.1555	2.05E-08	-0.1880	0.2875	5.13E-01	0.0457	0.0113	5.41E-05	0
rs9909861	17	47079416	18	47060322	47145848	A	C	0.3191	IGF2BP1	intronic	0.8659	0.1467	3.62E-09	0.0230	0.2812	9.35E-01	0.0458	0.0107	1.82E-05	0
rs12945020	17	47082775	18	47060322	47145848	A	G	0.3181	IGF2BP1:RP11-501	ncRNA_intronic	0.8547	0.1465	5.35E-09	0.0490	0.2810	8.62E-01	0.0435	0.0106	4.30E-05	0
rs35051752	17	47089908	18	47060322	47145848	A	G	0.3181	IGF2BP1:RP11-501	ncRNA_intronic	0.8605	0.1465	4.27E-09	0.0475	0.2809	8.66E-01	0.0430	0.0106	5.42E-05	0
rs11079849	17	47090785	18	47060322	47145848	T	C	0.2903	IGF2BP1:RP11-501	ncRNA_intronic	0.9559	0.1515	2.80E-10	0.2316	0.2877	4.21E-01	0.0443	0.0111	7.03E-05	0
rs9906710	17	47091283	18	47060322	47145848	A	C	0.3221	IGF2BP1	intronic	0.8553	0.1463	5.06E-09	0.0461	0.2803	8.69E-01	0.0425	0.0106	6.18E-05	0
rs9906944	17	47091420	18	47060322	47145848	T	C	0.2992	IGF2BP1	intronic	0.9051	0.1495	1.39E-09	-0.0506	0.2833	8.58E-01	0.0421	0.0110	1.23E-04	0
rs4794018	17	47093398	18	47060322	47145848	T	C	0.3191	IGF2BP1	intronic	-0.8486	0.1463	6.65E-09	-0.0365	0.2801	8.96E-01	-0.0425	0.0106	6.12E-05	0
rs9902512	17	47094274	18	47060322	47145848	C	G	0.3191	IGF2BP1	intronic	-0.8421	0.1465	8.92E-09	-0.0367	0.2801	8.96E-01	-0.0425	0.0106	6.26E-05	0
rs11079852	17	47095041	18	47060322	47145848	A	G	0.3201	IGF2BP1	intronic	0.8455	0.1463	7.53E-09	0.0382	0.2801	8.92E-01	0.0424	0.0106	6.22E-05	0

* Based on genome-wide tests of inferred statistics computed from the roi-specific GWASs of cortical surface area[1] in 19,152 participants of ENIGMA study[2].

** Replicated (=1) if the effect size estimates from both 'replication' association tests have the same direction as that from the meta-GWAS and p-values < 0.05.

1 .Nieuwboer, H. A., Pool, R., Dolan, C. V., Boomsma, D. I. & Nivard, M. G. GWIS: Genome-wide inferred statistics for functions of multiple phenotypes. The American Journal of Human Genetics 99, 917–927 (2016).

2. Grasby, K. L. et al. The genetic architecture of the human cerebral cortex. bioRxiv 399402 (2018). doi:10.1101/399402

Table E4B. GWAS meta-analysis results for surface area PC2 for SNPs with p <5E-08.

The table shows the genomic positions, alleles,mapped genes, and the functions with respect to the mapped genes. The association results are from the meta-GWAS; UKBB and ENIGMA cohorts.

											Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			
rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	Replicated**
rs1934057	1	18962095	19	18956404	18992466	T	C	0.4811	PAX7	intronic	-0.0762	0.0137	2.78E-08	-0.1065	0.0276	1.18E-04	-0.0662	0.0103	1.49E-10	1
rs9439716	1	18978263	19	18956404	18992466	A	C	0.4384	PAX7	intronic	0.0722	0.0131	3.96E-08	0.0817	0.0274	2.88E-03	0.0595	0.0099	1.97E-09	1
rs10917360	1	23539010	20	23473592	23543929	A	G	0.2495	HTR1D	intergenic	0.0829	0.0151	3.84E-08	0.1051	0.0312	7.62E-04	0.0355	0.0115	2.04E-03	1
rs7519093	1	23541078	20	23473592	23543929	A	T	0.2495	HTR1D	intergenic	0.0836	0.0151	3.03E-08	0.1075	0.0312	5.81E-04	0.0351	0.0115	2.29E-03	1
rs11801120	1	23543307	20	23473592	23543929	T	C	0.2495	HTR1D	intergenic	0.0834	0.0151	3.37E-08	0.1074	0.0312	5.87E-04	0.0354	0.0115	2.16E-03	1
rs7414010	1	23543929	20	23473592	23543929	T	C	0.2495	HTR1D	intergenic	-0.0832	0.0152	4.11E-08	-0.1065	0.0312	6.49E-04	-0.0346	0.0116	2.72E-03	1
rs4659441	1	26752992	21	26752992	26902694	T	C	0.2157	LIN28A	UTR3	-0.0972	0.0163	2.43E-09	-0.0369	0.0341	2.80E-01	-0.0499	0.0122	4.27E-05	0
rs9438623	1	26755919	21	26752992	26902694	A	G	0.1531	LIN28A	UTR3	-0.105	0.0181	6.21E-09	-0.0571	0.0385	1.38E-01	-0.0543	0.0137	7.85E-05	0
rs3811462	1	26758602	21	26752992	26902694	T	C	0.2177	DHDDS	upstream	-0.0953	0.0162	4.14E-09	-0.0383	0.0341	2.61E-01	-0.0481	0.0121	7.20E-05	0
rs9438550	1	26765576	21	26752992	26902694	T	C	0.2157	DHDDS	intronic	-0.0949	0.0162	5.07E-09	-0.0391	0.0341	2.52E-01	-0.0467	0.0121	1.15E-04	0
rs3127011	1	26782680	21	26752992	26902694	A	G	0.1511	DHDDS	intronic	-0.1034	0.0182	1.35E-08	-0.0467	0.0390	2.31E-01	-0.0494	0.0137	3.21E-04	0
rs2445639	1	26785926	21	26752992	26902694	A	G	0.1501	DHDDS	intronic	0.103	0.0182	1.64E-08	0.0466	0.0390	2.32E-01	0.0487	0.0138	4.29E-04	0
rs2445640	1	26788319	21	26752992	26902694	A	G	0.1501	DHDDS	intronic	-0.1032	0.0182	1.53E-08	-0.0468	0.0390	2.31E-01	-0.0492	0.0138	3.50E-04	0
rs2494391	1	26798478	21	26752992	26902694	T	C	0.2157	HMGN2	upstream:downs	-0.0955	0.0163	4.33E-09	-0.0341	0.0341	3.18E-01	-0.0449	0.0121	2.07E-04	0
rs2494399	1	26804796	21	26752992	26902694	C	G	0.2147	HMGN2	intergenic	-0.0948	0.0163	5.74E-09	-0.0326	0.0341	3.39E-01	-0.0457	0.0121	1.65E-04	0
rs2061234	1	26807312	21	26752992	26902694	A	G	0.1501	HMGN2	intergenic	0.1012	0.0183	3.19E-08	0.0466	0.0390	2.32E-01	0.0452	0.0139	1.16E-03	0
rs2445636	1	26808191	21	26752992	26902694	A	G	0.1491	HMGN2	intergenic	-0.1042	0.0183	1.16E-08	-0.0466	0.0390	2.32E-01	-0.0490	0.0138	4.01E-04	0
rs7543995	1	26814811	21	26752992	26902694	A	G	0.1501	HMGN2	intergenic	-0.1044	0.0183	1.17E-08	-0.0466	0.0390	2.32E-01	-0.0496	0.0139	3.48E-04	0
rs80117212	1	26841794	21	26752992	26902694	T	C	0.1531	DPPA2P2	intergenic	-0.1013	0.0183	3.07E-08	-0.0456	0.0390	2.42E-01	-0.0463	0.0138	7.62E-04	0
rs11589953	1	26851886	21	26752992	26902694	A	T	0.2177	RPS6KA1	intergenic	0.091	0.0163	2.28E-08	0.0289	0.0341	3.97E-01	0.0431	0.0121	3.64E-04	0
rs11247963	1	26855401	21	26752992	26902694	A	G	0.2177	RPS6KA1	upstream	-0.0909	0.0163	2.27E-08	-0.0286	0.0341	4.02E-01	-0.0421	0.0121	4.87E-04	0
rs2229714	1	26900708	21	26752992	26902694	A	G	0.1372	RPS6KA1	UTR3	-0.1051	0.0189	2.75E-08	-0.0272	0.0398	4.95E-01	-0.0432	0.0140	2.03E-03	0
rs12121702	1	26900805	21	26752992	26902694	A	G	0.1342	RPS6KA1	UTR3	-0.1055	0.0189	2.43E-08	-0.0265	0.0399	5.06E-01	-0.0432	0.0140	2.09E-03	0
rs351370	1	113054659	22	113054659	113252614	T	C	0.4006	WNT2B	intronic	0.0773	0.0138	1.94E-08	0.1068	0.0277	1.19E-04	0.0677	0.0106	1.44E-10	1
rs351372	1	113059220	22	113054659	113252614	A	T	0.4702	WNT2B	intronic	0.0783	0.0133	3.45E-09	0.1052	0.0275	1.30E-04	NA	NA	NA	NA
rs910697	1	113063125	22	113054659	113252614	A	G	0.4612	WNT2B	exonic	0.0833	0.0132	3.26E-10	0.1165	0.0275	2.32E-05	0.0700	0.0101	5.06E-12	1
rs12728001	1	113076756	22	113054659	113252614	T	C	0.4821	ST7L	intronic	0.0804	0.0131	9.02E-10	0.1038	0.0274	1.52E-04	0.0629	0.0100	3.02E-10	1
rs7512948	1	113081176	22	113054659	113252614	A	G	0.4761	ST7L	intronic	-0.0783	0.0131	2.20E-09	-0.0991	0.0273	2.85E-04	-0.0597	0.0100	2.55E-09	1
rs10776755	1	113082974	22	113054659	113252614	C	G	0.4751	ST7L	intronic	-0.0793	0.0132	1.68E-09	-0.0968	0.0273	4.01E-04	-0.0601	0.0100	2.12E-09	1
rs10745330	1	113083439	22	113054659	113252614	T	C	0.4811	ST7L	UTR3	-0.0799	0.013	8.87E-10	-0.1038	0.0274	1.51E-04	-0.0617	0.0099	5.39E-10	1
rs4838959	1	113085721	22	113054659	113252614	A	C	0.4712	ST7L	intronic	0.0752	0.0131	1.03E-08	0.0836	0.0273	2.23E-03	0.0588	0.0100	4.07E-09	1
rs7544663	1	113089006	22	113054659	113252614	T	C	0.4761	ST7L	intronic	-0.0776	0.013	2.34E-09	-0.0963	0.0274	4.40E-04	-0.0602	0.0099	1.23E-09	1
rs7513716	1	113089320	22	113054659	113252614	A	T	0.4761	ST7L	intronic	0.0775	0.013	2.41E-09	0.0962	0.0274	4.46E-04	NA	NA	NA	NA
rs10857963	1	113091487	22	113054659	113252614	T	C	0.4761	ST7L	intronic	-0.0776	0.013	2.33E-09	-0.0962	0.0274	4.46E-04	-0.0601	0.0099	1.31E-09	1
rs6537743	1	113092527	22	113054659	113252614	A	G	0.4761	ST7L	intronic	0.0777	0.013	2.25E-09	0.0961	0.0274	4.55E-04	0.0600	0.0099	1.38E-09	1
rs10776756	1	113098015	22	113054659	113252614	A	G	0.4761	ST7L	intronic	0.0818	0.0133	7.56E-10	0.0962	0.0274	4.45E-04	0.0603	0.0103	5.72E-09	1
rs12126277	1	113106369	22	113054659	113252614	A	G	0.4761	ST7L	intronic	0.0779	0.013	2.11E-09	0.0970	0.0274	3.98E-04	0.0600	0.0099	1.45E-09	1
rs507213	1	113109104	22	113054659	113252614	A	C	0.4801	ST7L	intronic	-0.0798	0.0133	1.89E-09	-0.0899	0.0273	9.94E-04	-0.0552	0.0103	7.42E-08	1
rs11102497	1	113109274	22	113054659	113252614	T	C	0.4761	ST7L	intronic	0.0787	0.013	1.54E-09	0.0959	0.0274	4.61E-04	0.0593	0.0100	2.55E-09	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs1001494	1	113110619	22	113054659	113252614	T	C	0.4761	ST7L	intronic	0.0793	0.013	1.19E-09	0.0981	0.0274	3.43E-04	0.0594	0.0100	2.49E-09	1
rs1032312	1	113112746	22	113054659	113252614	A	G	0.4761	ST7L	intronic	-0.0781	0.013	1.92E-09	-0.0959	0.0274	4.61E-04	-0.0596	0.0099	1.79E-09	1
rs10776757	1	113121673	22	113054659	113252614	C	G	0.4801	ST7L	intronic	-0.0762	0.013	5.18E-09	-0.0920	0.0273	7.47E-04	NA	NA	NA	NA
rs7554345	1	113122956	22	113054659	113252614	T	G	0.4742	ST7L	intronic	0.0777	0.013	2.33E-09	0.0969	0.0274	4.02E-04	0.0597	0.0099	1.70E-09	1
rs7554916	1	113123734	22	113054659	113252614	A	C	0.4732	ST7L	intronic	0.0778	0.013	2.28E-09	0.0969	0.0274	4.06E-04	0.0596	0.0099	1.83E-09	1
rs663533	1	113128804	22	113054659	113252614	C	G	0.4722	ST7L	intronic	-0.0742	0.0132	1.75E-08	-0.0845	0.0273	1.99E-03	-0.0586	0.0101	6.06E-09	1
rs6669096	1	113132361	22	113054659	113252614	T	C	0.4751	ST7L	intronic	0.0777	0.013	2.32E-09	0.0959	0.0274	4.64E-04	0.0594	0.0099	1.99E-09	1
rs6666579	1	113132393	22	113054659	113252614	A	G	0.4742	ST7L	intronic	0.0776	0.013	2.40E-09	0.0969	0.0274	4.05E-04	0.0594	0.0099	2.11E-09	1
rs6682737	1	113136229	22	113054659	113252614	T	C	0.4751	ST7L	intronic	0.0784	0.013	1.79E-09	0.0959	0.0274	4.66E-04	0.0609	0.0099	8.99E-10	1
rs4839254	1	113140926	22	113054659	113252614	T	C	0.4811	ST7L	intronic	-0.0758	0.013	5.98E-09	-0.0904	0.0273	9.26E-04	-0.0582	0.0100	5.50E-09	1
rs6691932	1	113144263	22	113054659	113252614	T	C	0.4851	ST7L	intronic	0.0766	0.013	3.98E-09	0.0963	0.0274	4.40E-04	0.0591	0.0099	2.82E-09	1
rs11102512	1	113145394	22	113054659	113252614	A	G	0.4742	ST7L	intronic	0.0774	0.013	2.80E-09	0.0973	0.0274	3.85E-04	0.0594	0.0099	2.17E-09	1
rs7522288	1	113151205	22	113054659	113252614	T	C	0.4583	ST7L	intronic	0.0746	0.0132	1.42E-08	0.0843	0.0274	2.06E-03	0.0584	0.0101	6.40E-09	1
rs7546094	1	113154400	22	113054659	113252614	T	C	0.4871	ST7L	intronic	-0.0767	0.013	3.74E-09	-0.0970	0.0274	4.02E-04	-0.0584	0.0100	4.44E-09	1
rs1994604	1	113156426	22	113054659	113252614	T	C	0.4871	ST7L	intronic	-0.0767	0.013	3.70E-09	-0.0970	0.0274	4.04E-04	-0.0584	0.0100	4.43E-09	1
rs6700673	1	113157054	22	113054659	113252614	T	C	0.4871	ST7L	intronic	-0.0766	0.013	3.88E-09	-0.0969	0.0274	4.10E-04	-0.0584	0.0100	4.41E-09	1
rs9429486	1	113157372	22	113054659	113252614	T	C	0.4692	ST7L	intronic	0.0748	0.013	9.31E-09	0.0928	0.0273	6.72E-04	0.0574	0.0100	9.95E-09	1
rs55675817	1	113166876	22	113054659	113252614	A	C	0.4583	CAPZA1	intronic	0.0749	0.0132	1.25E-08	0.0817	0.0273	2.83E-03	0.0578	0.0101	9.48E-09	1
rs7415820	1	113169449	22	113054659	113252614	A	G	0.4871	CAPZA1	intronic	0.077	0.013	3.15E-09	0.0947	0.0274	5.52E-04	0.0577	0.0100	6.72E-09	1
rs12046208	1	113171589	22	113054659	113252614	T	C	0.4682	CAPZA1	intronic	0.0749	0.013	8.78E-09	0.0919	0.0273	7.71E-04	0.0570	0.0100	1.21E-08	1
rs11584092	1	113176262	22	113054659	113252614	A	T	0.4682	CAPZA1	intronic	0.0764	0.0131	5.78E-09	0.0897	0.0273	1.03E-03	0.0587	0.0101	5.31E-09	1
rs72699100	1	113181401	22	113054659	113252614	A	G	0.4583	CAPZA1	intronic	-0.0754	0.0132	1.12E-08	-0.0842	0.0274	2.08E-03	-0.0582	0.0101	8.59E-09	1
rs12042407	1	113183879	22	113054659	113252614	A	T	0.4583	CAPZA1	intronic	-0.0766	0.0132	6.17E-09	-0.0832	0.0273	2.34E-03	-0.0583	0.0101	8.45E-09	1
rs3013440	1	113195789	22	113054659	113252614	A	G	0.4871	CAPZA1	intronic	0.0768	0.013	3.73E-09	0.0948	0.0274	5.51E-04	0.0577	0.0100	7.99E-09	1
rs3103450	1	113197730	22	113054659	113252614	A	G	0.4871	CAPZA1	intronic	0.0769	0.013	3.47E-09	0.0945	0.0274	5.73E-04	0.0578	0.0100	7.21E-09	1
rs7524494	1	113197800	22	113054659	113252614	A	G	0.4871	CAPZA1	intronic	-0.0768	0.013	3.58E-09	-0.0945	0.0274	5.73E-04	-0.0577	0.0100	7.96E-09	1
rs3013439	1	113200671	22	113054659	113252614	T	G	0.4871	CAPZA1	intronic	-0.077	0.013	3.36E-09	-0.0943	0.0274	5.82E-04	-0.0576	0.0100	8.11E-09	1
rs2932536	1	113202417	22	113054659	113252614	A	G	0.4871	CAPZA1	intronic	0.077	0.013	3.26E-09	0.0944	0.0274	5.74E-04	0.0575	0.0100	8.99E-09	1
rs12046329	1	113207531	22	113054659	113252614	T	C	0.4871	CAPZA1	intronic	-0.0781	0.013	2.13E-09	-0.0951	0.0274	5.23E-04	-0.0570	0.0100	1.22E-08	1
rs12046466	1	113208039	22	113054659	113252614	T	C	0.4871	CAPZA1	intronic	-0.0785	0.013	1.64E-09	-0.0952	0.0274	5.20E-04	-0.0578	0.0100	7.37E-09	1
rs6537749	1	113218503	22	113054659	113252614	T	C	0.4573	MOV10	intronic	-0.0762	0.0132	7.59E-09	-0.0864	0.0274	1.60E-03	-0.0577	0.0101	1.23E-08	1
rs2999155	1	113221658	22	113054659	113252614	A	G	0.4881	MOV10	intronic	0.0793	0.0131	1.22E-09	0.0958	0.0274	4.84E-04	0.0569	0.0100	1.34E-08	1
rs2999154	1	113222456	22	113054659	113252614	T	G	0.4881	MOV10	intronic	0.0786	0.013	1.68E-09	0.0972	0.0274	3.96E-04	0.0570	0.0100	1.33E-08	1
rs2999157	1	113233193	22	113054659	113252614	A	G	0.4871	MOV10	intronic	0.076	0.0131	7.49E-09	0.0980	0.0274	3.55E-04	0.0598	0.0102	3.83E-09	1
rs2932532	1	113234456	22	113054659	113252614	A	G	0.4881	MOV10	intronic	0.078	0.0131	2.54E-09	0.0976	0.0274	3.73E-04	0.0570	0.0101	1.51E-08	1
rs902289	1	113236087	22	113054659	113252614	T	C	0.4881	MOV10	intronic	0.0778	0.0131	2.79E-09	0.0973	0.0274	3.88E-04	0.0570	0.0101	1.50E-08	1
rs1110043	1	113236421	22	113054659	113252614	A	G	0.4583	MOV10:RP11-4	ncRNA_exonic	0.0746	0.0131	1.38E-08	0.0857	0.0273	1.73E-03	0.0559	0.0102	3.91E-08	1
rs2999158	1	113239478	22	113054659	113252614	T	C	0.334	MOV10	intronic	-0.0931	0.0139	2.13E-11	-0.1279	0.0291	1.09E-05	-0.0759	0.0108	1.76E-12	1
rs3013431	1	113242488	22	113054659	113252614	T	C	0.4016	MOV10	intronic	0.0803	0.0134	2.02E-09	0.1008	0.0281	3.40E-04	0.0660	0.0103	1.48E-10	1
rs937053	1	113246229	22	113054659	113252614	A	T	0.4543	RHOC:RP11-42	intronic	0.0746	0.0132	1.50E-08	0.0861	0.0276	1.80E-03	NA	NA	NA	NA
rs2999156	1	113247127	22	113054659	113252614	C	G	0.4543	RHOC:RP11-42	intronic	0.0761	0.0132	8.08E-09	0.0872	0.0275	1.56E-03	NA	NA	NA	NA

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs954679	1	113248365	22	113054659	113252614	A	G	0.3936	RHOC:RP11-42	UTR5	-0.0838	0.0134	4.38E-10	-0.1050	0.0283	2.10E-04	-0.0614	0.0104	3.43E-09	1
rs340496	2	45134871	23	45130410	45175585	C	G	0.4254	RP11-89K21.1	intergenic	0.0777	0.0132	4.57E-09	0.0727	0.0275	8.23E-03	0.0227	0.0101	2.44E-02	1
rs340497	2	45134900	23	45130410	45175585	C	G	0.4264	RP11-89K21.1	intergenic	0.078	0.0132	3.88E-09	0.0709	0.0275	1.00E-02	0.0228	0.0101	2.36E-02	1
rs340498	2	45135885	23	45130410	45175585	A	C	0.4334	RP11-89K21.1	intergenic	-0.0779	0.0133	4.48E-09	-0.0703	0.0274	1.05E-02	-0.0232	0.0101	2.15E-02	1
rs564906	2	45136693	23	45130410	45175585	C	G	0.4264	RP11-89K21.1	intergenic	0.0775	0.0133	5.48E-09	0.0687	0.0274	1.23E-02	0.0233	0.0101	2.12E-02	1
rs564207	2	45136742	23	45130410	45175585	T	C	0.4225	RP11-89K21.1	intergenic	-0.0793	0.0133	2.41E-09	-0.0694	0.0275	1.15E-02	-0.0219	0.0102	3.09E-02	1
rs540395	2	45138444	23	45130410	45175585	A	C	0.4165	RP11-89K21.1	intergenic	-0.0739	0.0134	3.80E-08	-0.0593	0.0279	3.37E-02	-0.0285	0.0102	5.25E-03	1
rs540606	2	45138507	23	45130410	45175585	A	G	0.4254	RP11-89K21.1	intergenic	-0.0781	0.0133	4.01E-09	-0.0708	0.0274	9.72E-03	-0.0236	0.0101	1.97E-02	1
rs567047	2	45139093	23	45130410	45175585	A	G	0.4225	RP11-89K21.1	intergenic	-0.0785	0.0133	3.42E-09	-0.0696	0.0274	1.11E-02	-0.0235	0.0101	2.03E-02	1
rs567897	2	45139153	23	45130410	45175585	A	G	0.4185	RP11-89K21.1	intergenic	-0.0733	0.0134	4.86E-08	-0.0570	0.0279	4.12E-02	-0.0274	0.0102	7.14E-03	1
rs473098	2	45139779	23	45130410	45175585	T	C	0.4235	RP11-89K21.1	intergenic	0.0782	0.0133	3.86E-09	0.0686	0.0273	1.21E-02	0.0234	0.0101	2.08E-02	1
rs472140	2	45139904	23	45130410	45175585	T	C	0.4205	RP11-89K21.1	intergenic	0.0792	0.0133	2.46E-09	0.0680	0.0274	1.30E-02	0.0235	0.0101	2.02E-02	1
rs518853	2	45141218	23	45130410	45175585	A	G	0.4205	RP11-89K21.1	intergenic	0.0799	0.0133	1.87E-09	0.0679	0.0274	1.33E-02	0.0236	0.0101	1.94E-02	1
rs570436	2	45142673	23	45130410	45175585	T	C	0.4225	RP11-89K21.1	intergenic	0.0784	0.0133	3.69E-09	0.0751	0.0275	6.31E-03	0.0243	0.0101	1.62E-02	1
rs578584	2	45143175	23	45130410	45175585	A	T	0.4245	RP11-89K21.1	intergenic	-0.0772	0.0133	6.43E-09	-0.0732	0.0275	7.83E-03	-0.0234	0.0101	2.08E-02	1
rs542883	2	45143382	23	45130410	45175585	C	G	0.4215	RP11-89K21.1	intergenic	0.0789	0.0133	2.99E-09	0.0690	0.0275	1.22E-02	0.0248	0.0101	1.42E-02	1
rs490340	2	45151616	23	45130410	45175585	T	C	0.4324	RP11-89K21.1	ncRNA_intronic	0.081	0.0133	1.27E-09	0.0710	0.0275	9.73E-03	0.0256	0.0101	1.15E-02	1
rs528301	2	45154908	23	45130410	45175585	A	G	0.4294	RP11-89K21.1	ncRNA_intronic	0.0844	0.0133	2.30E-10	0.0672	0.0274	1.43E-02	0.0249	0.0101	1.40E-02	1
rs1004787	2	45159091	23	45130410	45175585	A	G	0.4602	RP11-89K21.1	ncRNA_intronic	0.0813	0.0132	7.56E-10	0.0607	0.0273	2.63E-02	0.0218	0.0100	2.99E-02	1
rs895632	2	45165045	23	45130410	45175585	A	C	0.4324	RP11-89K21.1	ncRNA_intronic	-0.0811	0.0133	9.65E-10	-0.0505	0.0274	6.50E-02	-0.0281	0.0101	5.31E-03	0
rs1561227	2	45165389	23	45130410	45175585	T	C	0.4602	RP11-89K21.1	ncRNA_intronic	0.0805	0.0132	1.08E-09	0.0541	0.0272	4.70E-02	0.0265	0.0100	7.94E-03	1
rs83995	2	45167570	23	45130410	45175585	T	G	0.4095	SIX3-AS1	ncRNA_exonic	0.0851	0.0133	1.49E-10	0.0553	0.0277	4.63E-02	0.0285	0.0101	4.59E-03	1
rs741813	2	45167886	23	45130410	45175585	A	T	0.4602	SIX3-AS1	ncRNA_exonic	0.0814	0.0132	6.93E-10	0.0592	0.0273	2.99E-02	0.0269	0.0100	7.17E-03	1
rs338070	2	45175289	23	45130410	45175585	C	G	0.4076	SIX3	intergenic	-0.0812	0.0133	1.12E-09	-0.0587	0.0279	3.55E-02	-0.0288	0.0102	4.86E-03	1
rs173076	2	45175585	23	45130410	45175585	A	G	0.4105	SIX3	intergenic	0.0811	0.0133	1.13E-09	0.0579	0.0279	3.81E-02	0.0295	0.0102	3.92E-03	1
rs4895120	3	104647183	24	104646815	104828166	T	C	0.493	RP11-281P11.1	intergenic	-0.1009	0.0132	1.93E-14	-0.0965	0.0272	3.86E-04	-0.0689	0.0101	1.04E-11	1
rs9826055	3	104647968	24	104646815	104828166	A	T	0.493	RP11-281P11.1	intergenic	-0.1009	0.0132	1.88E-14	-0.0953	0.0272	4.54E-04	NA	NA	NA	NA
rs2196494	3	104650052	24	104646815	104828166	T	C	0.4911	RP11-281P11.1	intergenic	-0.1015	0.0132	1.41E-14	-0.0954	0.0271	4.40E-04	-0.0688	0.0101	1.12E-11	1
rs12695100	3	104650477	24	104646815	104828166	T	C	0.4911	RP11-281P11.1	intergenic	-0.1008	0.0131	1.64E-14	-0.0954	0.0271	4.42E-04	-0.0683	0.0101	1.29E-11	1
rs6794834	3	104651280	24	104646815	104828166	T	C	0.4911	RP11-281P11.1	intergenic	0.1009	0.0131	1.55E-14	0.0945	0.0271	5.00E-04	0.0683	0.0101	1.29E-11	1
rs4264756	3	104651489	24	104646815	104828166	C	G	0.493	RP11-281P11.1	intergenic	-0.1008	0.0131	1.56E-14	-0.0945	0.0271	5.02E-04	NA	NA	NA	NA
rs1540462	3	104651985	24	104646815	104828166	A	G	0.493	RP11-281P11.1	intergenic	-0.1009	0.0131	1.48E-14	-0.0956	0.0271	4.28E-04	-0.0681	0.0101	1.39E-11	1
rs1910326	3	104652528	24	104646815	104828166	T	C	0.492	RP11-281P11.1	intergenic	-0.1009	0.0131	1.42E-14	-0.0953	0.0271	4.44E-04	-0.0680	0.0101	1.41E-11	1
rs4895122	3	104652961	24	104646815	104828166	A	G	0.1978	RP11-281P11.1	intergenic	0.1008	0.0164	7.83E-10	0.0789	0.0345	2.21E-02	0.0618	0.0125	7.17E-07	1
rs993463	3	104653545	24	104646815	104828166	A	T	0.492	RP11-281P11.1	intergenic	-0.1015	0.0131	9.65E-15	-0.0953	0.0271	4.41E-04	NA	NA	NA	NA
rs6780351	3	104654075	24	104646815	104828166	A	C	0.4911	ALCAM	intergenic	-0.0999	0.0131	2.66E-14	-0.0951	0.0271	4.54E-04	-0.0682	0.0101	1.36E-11	1
rs12490814	3	104654515	24	104646815	104828166	T	C	0.4891	ALCAM	intergenic	-0.1012	0.0131	1.17E-14	-0.0966	0.0271	3.71E-04	-0.0674	0.0100	1.90E-11	1
rs7649239	3	104654791	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	0.1007	0.0131	1.45E-14	0.0953	0.0271	4.41E-04	0.0669	0.0100	1.85E-11	1
rs2043626	3	104655212	24	104646815	104828166	T	C	0.492	ALCAM	intergenic	0.1007	0.0131	1.45E-14	0.0954	0.0271	4.36E-04	0.0668	0.0099	1.78E-11	1
rs6808509	3	104655582	24	104646815	104828166	A	C	0.4911	ALCAM	intergenic	0.0986	0.013	3.55E-14	0.0951	0.0271	4.57E-04	0.0665	0.0099	1.73E-11	1
rs6773136	3	104655765	24	104646815	104828166	T	C	0.4911	ALCAM	intergenic	-0.0986	0.013	3.56E-14	-0.0950	0.0271	4.60E-04	-0.0666	0.0099	1.68E-11	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs6808909	3	104655818	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	0.0986	0.013	3.59E-14	0.0951	0.0271	4.56E-04	0.0666	0.0099	1.71E-11	1
rs2118003	3	104656639	24	104646815	104828166	A	C	0.4911	ALCAM	intergenic	0.0988	0.013	3.26E-14	0.0952	0.0271	4.52E-04	0.0666	0.0099	1.63E-11	1
rs2118004	3	104656715	24	104646815	104828166	T	C	0.4911	ALCAM	intergenic	0.0986	0.013	3.64E-14	0.0953	0.0271	4.40E-04	0.0666	0.0099	1.70E-11	1
rs6766559	3	104656989	24	104646815	104828166	C	G	0.492	ALCAM	intergenic	0.0986	0.013	3.67E-14	0.0957	0.0271	4.20E-04	NA	NA	NA	NA
rs6766724	3	104657313	24	104646815	104828166	C	G	0.4901	ALCAM	intergenic	-0.0987	0.013	3.36E-14	-0.0963	0.0271	3.87E-04	NA	NA	NA	NA
rs11713472	3	104657409	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	-0.098	0.013	5.54E-14	-0.0953	0.0271	4.39E-04	-0.0662	0.0099	2.73E-11	1
rs6783013	3	104658328	24	104646815	104828166	T	C	0.2813	ALCAM	intergenic	-0.0895	0.0146	9.71E-10	-0.0501	0.0303	9.81E-02	-0.0719	0.0111	9.20E-11	0
rs76664757	3	104660317	24	104646815	104828166	A	T	0.1968	ALCAM	intergenic	-0.1005	0.0164	8.14E-10	-0.0794	0.0345	2.13E-02	-0.0624	0.0124	4.90E-07	1
rs13077489	3	104660608	24	104646815	104828166	C	G	0.3062	ALCAM	intergenic	0.0845	0.0155	4.58E-08	0.0968	0.0298	1.18E-03	0.0582	0.0119	1.06E-06	1
rs9829580	3	104660892	24	104646815	104828166	A	G	0.4901	ALCAM	intergenic	0.0987	0.013	3.39E-14	0.0964	0.0271	3.78E-04	0.0666	0.0099	1.62E-11	1
rs9867223	3	104661131	24	104646815	104828166	A	T	0.4901	ALCAM	intergenic	-0.0987	0.013	3.35E-14	-0.0964	0.0271	3.78E-04	NA	NA	NA	NA
rs9868127	3	104661750	24	104646815	104828166	A	G	0.4901	ALCAM	intergenic	-0.0989	0.013	2.93E-14	-0.0964	0.0271	3.83E-04	-0.0667	0.0099	1.50E-11	1
rs13318870	3	104662433	24	104646815	104828166	T	C	0.4901	ALCAM	intergenic	0.0987	0.013	3.22E-14	0.0966	0.0271	3.72E-04	0.0666	0.0099	1.63E-11	1
rs77652765	3	104663554	24	104646815	104828166	A	G	0.1978	ALCAM	intergenic	0.1002	0.0163	8.67E-10	0.0782	0.0345	2.33E-02	0.0631	0.0124	3.67E-07	1
rs7618943	3	104664130	24	104646815	104828166	A	C	0.4901	ALCAM	intergenic	0.0985	0.013	3.76E-14	0.0938	0.0271	5.52E-04	0.0669	0.0099	1.39E-11	1
rs1393740	3	104664955	24	104646815	104828166	A	C	0.4901	ALCAM	intergenic	0.0982	0.013	4.36E-14	0.0938	0.0271	5.46E-04	0.0674	0.0099	9.25E-12	1
rs1393741	3	104664981	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	0.0986	0.013	3.50E-14	0.0963	0.0271	3.88E-04	0.0672	0.0099	1.10E-11	1
rs6792637	3	104666491	24	104646815	104828166	T	C	0.4274	ALCAM	intergenic	-0.0752	0.0132	1.28E-08	-0.0528	0.0273	5.27E-02	-0.0627	0.0100	4.48E-10	0
rs6782467	3	104666925	24	104646815	104828166	T	C	0.493	ALCAM	intergenic	0.099	0.013	2.63E-14	0.0969	0.0271	3.58E-04	0.0667	0.0099	1.53E-11	1
rs6782636	3	104666928	24	104646815	104828166	C	G	0.493	ALCAM	intergenic	0.0986	0.013	3.46E-14	0.0971	0.0271	3.42E-04	NA	NA	NA	NA
rs6806605	3	104666970	24	104646815	104828166	A	C	0.4911	ALCAM	intergenic	-0.0986	0.013	3.38E-14	-0.0948	0.0271	4.71E-04	-0.0667	0.0099	1.47E-11	1
rs13066237	3	104666976	24	104646815	104828166	T	C	0.4245	ALCAM	intergenic	0.0951	0.0132	5.04E-13	0.1088	0.0274	7.11E-05	0.0512	0.0100	3.41E-07	1
rs12492893	3	104667061	24	104646815	104828166	T	G	0.4274	ALCAM	intergenic	-0.0752	0.0132	1.29E-08	-0.0528	0.0273	5.25E-02	-0.0628	0.0100	4.11E-10	0
rs12374063	3	104667506	24	104646815	104828166	A	C	0.4891	ALCAM	intergenic	0.099	0.013	3.21E-14	0.0978	0.0271	3.12E-04	0.0669	0.0099	1.63E-11	1
rs12374161	3	104667530	24	104646815	104828166	A	T	0.4891	ALCAM	intergenic	-0.099	0.013	3.29E-14	-0.0957	0.0271	4.16E-04	NA	NA	NA	NA
rs6807218	3	104667576	24	104646815	104828166	A	G	0.1958	ALCAM	intergenic	0.1004	0.0164	8.48E-10	0.0784	0.0344	2.27E-02	0.0629	0.0124	4.03E-07	1
rs12374067	3	104667829	24	104646815	104828166	A	G	0.4901	ALCAM	intergenic	0.1008	0.0131	1.20E-14	0.0972	0.0271	3.36E-04	0.0671	0.0099	1.40E-11	1
rs13092127	3	104667944	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	-0.1008	0.0131	1.18E-14	-0.0972	0.0271	3.35E-04	-0.0672	0.0099	1.35E-11	1
rs35266846	3	104668010	24	104646815	104828166	T	C	0.4911	ALCAM	intergenic	0.102	0.0131	5.84E-15	0.0974	0.0271	3.30E-04	0.0670	0.0099	1.47E-11	1
rs35569867	3	104668074	24	104646815	104828166	T	G	0.4911	ALCAM	intergenic	-0.1008	0.0131	1.23E-14	-0.0951	0.0271	4.54E-04	-0.0671	0.0099	1.40E-11	1
rs9839056	3	104668172	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	0.1008	0.0131	1.17E-14	0.0972	0.0271	3.35E-04	0.0672	0.0099	1.33E-11	1
rs9876402	3	104668183	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	-0.1009	0.0131	1.11E-14	-0.0973	0.0271	3.34E-04	-0.0672	0.0099	1.32E-11	1
rs9839153	3	104668453	24	104646815	104828166	C	G	0.492	ALCAM	intergenic	-0.1011	0.0131	1.07E-14	-0.0973	0.0271	3.34E-04	NA	NA	NA	NA
rs6789712	3	104669023	24	104646815	104828166	T	G	0.4264	ALCAM	intergenic	0.0753	0.0132	1.24E-08	0.0538	0.0272	4.86E-02	0.0633	0.0101	4.41E-10	1
rs1436337	3	104669238	24	104646815	104828166	T	C	0.4911	ALCAM	intergenic	0.1013	0.0131	9.09E-15	0.0971	0.0271	3.44E-04	0.0674	0.0099	1.18E-11	1
rs7646958	3	104669766	24	104646815	104828166	T	C	0.492	ALCAM	intergenic	-0.1011	0.0131	1.00E-14	-0.0971	0.0271	3.42E-04	-0.0677	0.0099	9.56E-12	1
rs10804436	3	104670412	24	104646815	104828166	A	C	0.4274	ALCAM	intergenic	-0.0955	0.0132	3.99E-13	-0.1091	0.0274	6.77E-05	-0.0515	0.0101	3.85E-07	1
rs1816547	3	104670606	24	104646815	104828166	T	G	0.4911	ALCAM	intergenic	0.1009	0.0131	1.09E-14	0.0973	0.0271	3.35E-04	0.0670	0.0099	1.60E-11	1
rs6802252	3	104670860	24	104646815	104828166	A	T	0.4911	ALCAM	intergenic	-0.1007	0.0131	1.27E-14	-0.0948	0.0271	4.71E-04	NA	NA	NA	NA
rs1393742	3	104672111	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	-0.1008	0.0131	1.23E-14	-0.0974	0.0271	3.31E-04	-0.0670	0.0099	1.63E-11	1
rs1393743	3	104672291	24	104646815	104828166	A	C	0.4911	ALCAM	intergenic	-0.0999	0.0131	2.17E-14	-0.0953	0.0271	4.43E-04	-0.0668	0.0099	1.83E-11	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs9860835	3	104672414	24	104646815	104828166	T	G	0.4911	ALCAM	intergenic	0.1006	0.0131	1.42E-14	0.0974	0.0271	3.34E-04	0.0670	0.0099	1.63E-11	1
rs9823410	3	104672758	24	104646815	104828166	A	T	0.4911	ALCAM	intergenic	-0.1007	0.0131	1.36E-14	-0.0972	0.0271	3.43E-04	NA	NA	NA	NA
rs76521431	3	104672841	24	104646815	104828166	T	G	0.1968	ALCAM	intergenic	-0.1004	0.0163	8.11E-10	-0.0791	0.0344	2.15E-02	-0.0628	0.0124	3.93E-07	1
rs1436336	3	104673566	24	104646815	104828166	A	T	0.1968	ALCAM	intergenic	-0.1001	0.0163	9.02E-10	-0.0785	0.0344	2.25E-02	-0.0632	0.0124	3.34E-07	1
rs6788676	3	104674040	24	104646815	104828166	A	G	0.3638	ALCAM	intergenic	0.1062	0.0136	5.31E-15	0.0884	0.0281	1.65E-03	0.0679	0.0103	5.26E-11	1
rs112113804	3	104674454	24	104646815	104828166	A	G	0.1968	ALCAM	intergenic	-0.1011	0.0164	7.17E-10	-0.0794	0.0344	2.10E-02	-0.0631	0.0125	4.02E-07	1
rs79003825	3	104676223	24	104646815	104828166	A	C	0.2137	ALCAM	intergenic	-0.1105	0.0158	2.73E-12	-0.0573	0.0333	8.54E-02	-0.0729	0.0120	1.25E-09	0
rs7618202	3	104676606	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	-0.1006	0.0131	1.40E-14	-0.0979	0.0272	3.12E-04	-0.0661	0.0100	4.00E-11	1
rs2062774	3	104677139	24	104646815	104828166	T	C	0.2137	ALCAM	intergenic	0.1103	0.0158	2.90E-12	0.0573	0.0333	8.56E-02	0.0726	0.0120	1.47E-09	0
rs9863836	3	104678133	24	104646815	104828166	T	C	0.2137	ALCAM	intergenic	-0.1111	0.0159	2.61E-12	-0.0573	0.0336	8.84E-02	-0.0729	0.0120	1.28E-09	0
rs9863841	3	104678135	24	104646815	104828166	T	C	0.2137	ALCAM	intergenic	-0.111	0.0159	2.82E-12	-0.0570	0.0336	9.00E-02	-0.0731	0.0120	1.24E-09	0
rs12639074	3	104681496	24	104646815	104828166	T	C	0.4543	ALCAM	intergenic	0.0812	0.0133	9.77E-10	0.0962	0.0274	4.37E-04	0.0514	0.0102	4.97E-07	1
rs74546871	3	104682814	24	104646815	104828166	T	C	0.2137	ALCAM	intergenic	0.1104	0.0158	2.64E-12	0.0600	0.0333	7.14E-02	0.0737	0.0120	8.03E-10	0
rs11915534	3	104682872	24	104646815	104828166	A	C	0.3648	ALCAM	intergenic	-0.0835	0.0137	9.64E-10	-0.0547	0.0282	5.25E-02	-0.0601	0.0105	1.07E-08	0
rs9288795	3	104683753	24	104646815	104828166	T	C	0.4443	ALCAM	intergenic	-0.1044	0.0131	1.72E-15	-0.0923	0.0273	7.27E-04	-0.0606	0.0101	1.76E-09	1
rs7625683	3	104687585	24	104646815	104828166	T	C	0.2137	ALCAM	intergenic	0.1103	0.0158	2.83E-12	0.0597	0.0333	7.27E-02	0.0741	0.0120	6.40E-10	0
rs13086204	3	104687952	24	104646815	104828166	A	T	0.4911	ALCAM	intergenic	0.0999	0.0131	2.49E-14	0.0971	0.0272	3.59E-04	NA	NA	NA	NA
rs9850952	3	104688036	24	104646815	104828166	A	G	0.2137	ALCAM	intergenic	0.1103	0.0158	2.86E-12	0.0598	0.0333	7.26E-02	0.0744	0.0120	5.42E-10	0
rs4894893	3	104691743	24	104646815	104828166	T	C	0.2137	ALCAM	intergenic	-0.1103	0.0158	2.69E-12	-0.0596	0.0333	7.32E-02	-0.0744	0.0120	5.56E-10	0
rs4894894	3	104691806	24	104646815	104828166	T	C	0.4443	ALCAM	intergenic	0.1039	0.0131	2.33E-15	0.0924	0.0273	7.19E-04	0.0607	0.0101	1.68E-09	1
rs34044746	3	104692695	24	104646815	104828166	T	C	0.4443	ALCAM	intergenic	-0.1037	0.0131	2.56E-15	-0.0927	0.0273	6.96E-04	-0.0609	0.0101	1.52E-09	1
rs13319705	3	104693252	24	104646815	104828166	T	C	0.2942	ALCAM	intergenic	-0.1186	0.0141	4.70E-17	-0.0986	0.0297	8.89E-04	-0.0655	0.0108	1.33E-09	1
rs9846639	3	104694609	24	104646815	104828166	A	G	0.2137	ALCAM	intergenic	-0.1099	0.0158	3.31E-12	-0.0597	0.0333	7.29E-02	-0.0743	0.0120	5.86E-10	0
rs13320037	3	104694900	24	104646815	104828166	T	G	0.2942	ALCAM	intergenic	0.1186	0.0141	4.55E-17	0.0987	0.0297	8.82E-04	0.0654	0.0108	1.38E-09	1
rs9827968	3	104695956	24	104646815	104828166	A	G	0.4911	ALCAM	intergenic	0.0998	0.0131	2.79E-14	0.0971	0.0272	3.60E-04	0.0675	0.0100	1.77E-11	1
rs79588215	3	104697042	24	104646815	104828166	T	C	0.2137	ALCAM	intergenic	0.1104	0.0158	2.70E-12	0.0604	0.0333	6.94E-02	0.0742	0.0120	5.86E-10	0
rs1354281	3	104697513	24	104646815	104828166	A	G	0.4443	ALCAM	intergenic	-0.1035	0.0132	3.88E-15	-0.0926	0.0273	6.98E-04	-0.0599	0.0101	3.24E-09	1
rs9854793	3	104701066	24	104646815	104828166	A	G	0.2137	ALCAM	intergenic	-0.1101	0.0158	3.00E-12	-0.0605	0.0333	6.90E-02	-0.0741	0.0120	6.08E-10	0
rs9880189	3	104702294	24	104646815	104828166	T	C	0.4443	ALCAM	intergenic	0.1037	0.0131	2.62E-15	0.0928	0.0273	6.87E-04	0.0601	0.0100	1.89E-09	1
rs28374795	3	104702921	24	104646815	104828166	A	G	0.2137	ALCAM	intergenic	0.112	0.0158	1.58E-12	0.0608	0.0333	6.77E-02	0.0730	0.0120	1.15E-09	0
rs6771251	3	104704039	24	104646815	104828166	T	C	0.4443	ALCAM	intergenic	-0.1039	0.0131	2.34E-15	-0.0937	0.0273	6.08E-04	-0.0601	0.0100	1.87E-09	1
rs9846552	3	104705960	24	104646815	104828166	T	C	0.4443	ALCAM	intergenic	0.1038	0.0131	2.35E-15	0.0936	0.0273	6.12E-04	0.0600	0.0100	2.03E-09	1
rs1818149	3	104711110	24	104646815	104828166	T	C	0.4423	ALCAM	intergenic	0.1026	0.0131	3.81E-15	0.0918	0.0273	7.82E-04	0.0594	0.0101	3.43E-09	1
rs1354280	3	104711433	24	104646815	104828166	A	G	0.4414	ALCAM	intergenic	0.1017	0.0131	6.88E-15	0.0908	0.0273	8.88E-04	0.0583	0.0101	8.13E-09	1
rs9854000	3	104711549	24	104646815	104828166	T	C	0.4423	ALCAM	intergenic	-0.1022	0.0131	4.95E-15	-0.0921	0.0273	7.45E-04	-0.0594	0.0101	3.69E-09	1
rs9808934	3	104713251	24	104646815	104828166	T	G	0.2157	ALCAM	intergenic	0.1098	0.0157	2.60E-12	0.0611	0.0332	6.63E-02	0.0738	0.0119	6.30E-10	0
rs957485	3	104713687	24	104646815	104828166	T	C	0.2137	ALCAM	intergenic	-0.1095	0.0157	3.01E-12	-0.0608	0.0332	6.75E-02	-0.0732	0.0119	7.94E-10	0
rs12495603	3	104713881	24	104646815	104828166	A	G	0.492	ALCAM	intergenic	0.0995	0.0131	3.41E-14	0.0975	0.0272	3.42E-04	0.0663	0.0100	3.48E-11	1
rs4894822	3	104714106	24	104646815	104828166	A	C	0.4443	ALCAM	intergenic	-0.0999	0.0131	2.34E-14	-0.0921	0.0273	7.44E-04	-0.0540	0.0102	1.08E-07	1
rs9869633	3	104714210	24	104646815	104828166	A	G	0.2167	ALCAM	intergenic	-0.11	0.0157	2.41E-12	-0.0611	0.0332	6.62E-02	-0.0739	0.0119	5.63E-10	0
rs13327829	3	104714898	24	104646815	104828166	A	G	0.2157	ALCAM	intergenic	0.11	0.0157	2.34E-12	0.0611	0.0332	6.62E-02	0.0745	0.0119	3.95E-10	0

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs13324580	3	104715038	24	104646815	104828166	T	C	0.2127	ALCAM	intergenic	0.11	0.0157	2.46E-12	0.0601	0.0333	7.09E-02	0.0740	0.0119	5.44E-10	0
rs6769796	3	104715856	24	104646815	104828166	A	G	0.4443	ALCAM	intergenic	0.1031	0.013	2.72E-15	0.0935	0.0273	6.24E-04	0.0593	0.0101	4.03E-09	1
rs6769805	3	104715884	24	104646815	104828166	A	C	0.2157	ALCAM	intergenic	0.1098	0.0157	2.63E-12	0.0611	0.0332	6.62E-02	0.0748	0.0119	3.58E-10	0
rs59016227	3	104716337	24	104646815	104828166	T	G	0.2157	ALCAM	intergenic	-0.109	0.0157	4.29E-12	-0.0611	0.0332	6.62E-02	-0.0745	0.0120	5.69E-10	0
rs58911379	3	104716969	24	104646815	104828166	A	T	0.2167	ALCAM	intergenic	-0.1096	0.0157	2.87E-12	-0.0630	0.0332	5.79E-02	-0.0747	0.0119	3.52E-10	0
rs13327531	3	104718011	24	104646815	104828166	T	C	0.4443	ALCAM	intergenic	0.1032	0.013	2.59E-15	0.0937	0.0273	6.11E-04	0.0590	0.0101	4.69E-09	1
rs6802022	3	104718523	24	104646815	104828166	A	G	0.2157	ALCAM	intergenic	-0.11	0.0157	2.38E-12	-0.0611	0.0332	6.63E-02	-0.0753	0.0119	2.38E-10	0
rs10222610	3	104719661	24	104646815	104828166	A	G	0.2157	ALCAM	intergenic	-0.11	0.0157	2.37E-12	-0.0608	0.0332	6.76E-02	-0.0754	0.0119	2.34E-10	0
rs10222621	3	104719857	24	104646815	104828166	T	C	0.2157	ALCAM	intergenic	-0.11	0.0157	2.38E-12	-0.0611	0.0332	6.62E-02	-0.0754	0.0119	2.36E-10	0
rs10222454	3	104719975	24	104646815	104828166	A	G	0.2167	ALCAM	intergenic	0.1103	0.0157	2.08E-12	0.0631	0.0332	5.77E-02	0.0757	0.0119	2.01E-10	0
rs10222457	3	104720112	24	104646815	104828166	A	C	0.4443	ALCAM	intergenic	0.1024	0.013	4.26E-15	0.0934	0.0273	6.34E-04	0.0589	0.0101	5.04E-09	1
rs10222624	3	104720126	24	104646815	104828166	A	G	0.1889	ALCAM	intergenic	-0.1064	0.0169	3.28E-10	-0.0482	0.0357	1.77E-01	-0.0769	0.0128	2.13E-09	0
rs72989330	3	104721389	24	104646815	104828166	T	G	0.2157	ALCAM	intergenic	-0.11	0.0157	2.38E-12	-0.0610	0.0333	6.68E-02	-0.0754	0.0119	2.43E-10	0
rs72989332	3	104721814	24	104646815	104828166	T	C	0.2157	ALCAM	intergenic	-0.11	0.0157	2.36E-12	-0.0610	0.0333	6.68E-02	-0.0754	0.0119	2.45E-10	0
rs11929686	3	104722114	24	104646815	104828166	A	G	0.4443	ALCAM	intergenic	-0.1024	0.013	4.04E-15	-0.0926	0.0273	7.02E-04	-0.0587	0.0100	4.34E-09	1
rs6772884	3	104722492	24	104646815	104828166	A	C	0.2157	ALCAM	intergenic	0.111	0.0157	1.79E-12	0.0610	0.0333	6.67E-02	0.0749	0.0120	4.27E-10	0
rs6797921	3	104722799	24	104646815	104828166	A	G	0.2157	ALCAM	intergenic	-0.11	0.0157	2.46E-12	-0.0607	0.0333	6.83E-02	-0.0751	0.0119	2.71E-10	0
rs1393744	3	104722954	24	104646815	104828166	T	C	0.2157	ALCAM	intergenic	0.1101	0.0157	2.38E-12	0.0610	0.0333	6.69E-02	0.0744	0.0119	3.42E-10	0
rs72989334	3	104723673	24	104646815	104828166	T	G	0.2197	ALCAM	intergenic	-0.1118	0.0156	8.36E-13	-0.0603	0.0331	6.81E-02	-0.0767	0.0118	8.45E-11	0
rs7647615	3	104723971	24	104646815	104828166	C	G	0.492	ALCAM	intergenic	0.0973	0.0134	4.20E-13	0.0978	0.0273	3.33E-04	NA	NA	NA	NA
rs9839209	3	104724315	24	104646815	104828166	T	G	0.2157	ALCAM	intergenic	0.1102	0.0157	2.23E-12	0.0610	0.0333	6.68E-02	0.0744	0.0119	3.48E-10	0
rs971551	3	104724634	24	104646815	104828166	T	C	0.2157	ALCAM	intergenic	-0.1102	0.0157	2.26E-12	-0.0623	0.0333	6.13E-02	-0.0743	0.0119	3.64E-10	0
rs971550	3	104724787	24	104646815	104828166	A	T	0.2972	ALCAM	intergenic	0.1192	0.0141	2.54E-17	0.1001	0.0297	7.50E-04	0.0675	0.0107	2.57E-10	1
rs4894896	3	104726660	24	104646815	104828166	A	G	0.2117	ALCAM	intergenic	0.1098	0.0157	2.98E-12	0.0593	0.0333	7.48E-02	0.0735	0.0119	5.92E-10	0
rs4894897	3	104726699	24	104646815	104828166	C	G	0.1899	ALCAM	intergenic	-0.1071	0.017	2.69E-10	-0.0504	0.0357	1.58E-01	-0.0785	0.0128	8.13E-10	0
rs72989338	3	104727420	24	104646815	104828166	T	C	0.1879	ALCAM	intergenic	-0.1058	0.017	4.55E-10	-0.0488	0.0357	1.72E-01	-0.0780	0.0128	1.08E-09	0
rs6766074	3	104727505	24	104646815	104828166	C	G	0.1879	ALCAM	intergenic	-0.1056	0.017	4.82E-10	-0.0504	0.0357	1.58E-01	-0.0780	0.0128	1.05E-09	0
rs1604640	3	104728491	24	104646815	104828166	C	G	0.1879	ALCAM	intergenic	0.1055	0.017	5.06E-10	0.0490	0.0357	1.70E-01	0.0779	0.0128	1.15E-09	0
rs6769723	3	104728781	24	104646815	104828166	A	G	0.1879	ALCAM	intergenic	-0.1053	0.017	5.37E-10	-0.0504	0.0357	1.58E-01	-0.0780	0.0128	1.09E-09	0
rs6796574	3	104728944	24	104646815	104828166	A	G	0.1879	ALCAM	intergenic	0.1053	0.017	5.36E-10	0.0506	0.0357	1.56E-01	0.0780	0.0128	1.10E-09	0
rs6785288	3	104729083	24	104646815	104828166	T	C	0.1859	ALCAM	intergenic	0.1055	0.017	5.11E-10	0.0482	0.0357	1.78E-01	0.0775	0.0128	1.36E-09	0
rs6772559	3	104729180	24	104646815	104828166	A	G	0.4175	ALCAM	intergenic	-0.0927	0.0132	2.00E-12	-0.0824	0.0276	2.82E-03	-0.0555	0.0101	3.83E-08	1
rs17386778	3	104729589	24	104646815	104828166	A	T	0.4175	ALCAM	intergenic	-0.0926	0.0132	2.14E-12	-0.0827	0.0276	2.72E-03	-0.0554	0.0101	3.98E-08	1
rs9682035	3	104730056	24	104646815	104828166	T	G	0.4175	ALCAM	intergenic	0.0925	0.0132	2.30E-12	0.0827	0.0276	2.72E-03	0.0556	0.0101	3.56E-08	1
rs9682661	3	104730312	24	104646815	104828166	A	G	0.4175	ALCAM	intergenic	0.0921	0.0132	3.01E-12	0.0827	0.0276	2.74E-03	0.0544	0.0101	7.88E-08	1
rs9288796	3	104730581	24	104646815	104828166	A	G	0.1879	ALCAM	intergenic	-0.1055	0.017	5.00E-10	-0.0489	0.0357	1.71E-01	-0.0763	0.0129	2.95E-09	0
rs4894898	3	104732673	24	104646815	104828166	A	G	0.1879	ALCAM	intergenic	-0.1046	0.017	7.25E-10	-0.0495	0.0357	1.66E-01	-0.0769	0.0128	1.73E-09	0
rs9838717	3	104732961	24	104646815	104828166	T	G	0.1769	ALCAM	intergenic	-0.11	0.0172	1.66E-10	-0.0485	0.0364	1.83E-01	-0.0772	0.0129	1.95E-09	0
rs9858732	3	104733096	24	104646815	104828166	A	T	0.1769	ALCAM	intergenic	-0.1098	0.0172	1.75E-10	-0.0487	0.0364	1.80E-01	-0.0767	0.0129	2.40E-09	0
rs72989342	3	104733118	24	104646815	104828166	T	G	0.1789	ALCAM	intergenic	0.1098	0.0172	1.73E-10	0.0512	0.0363	1.58E-01	0.0771	0.0129	2.04E-09	0
rs28578901	3	104733192	24	104646815	104828166	T	C	0.1769	ALCAM	intergenic	0.1097	0.0172	1.79E-10	0.0476	0.0364	1.90E-01	0.0766	0.0129	2.60E-09	0

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs16850758	3	104733368	24	104646815	104828166	T	C	0.1779	ALCAM	intergenic	0.1092	0.0172	2.16E-10	0.0498	0.0363	1.70E-01	0.0765	0.0129	2.68E-09	0
rs16850761	3	104733455	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	0.1087	0.0172	2.61E-10	0.0500	0.0363	1.69E-01	0.0766	0.0129	2.58E-09	0
rs16850762	3	104733601	24	104646815	104828166	T	C	0.1769	ALCAM	intergenic	0.1087	0.0172	2.67E-10	0.0512	0.0363	1.59E-01	0.0766	0.0129	2.58E-09	0
rs16850763	3	104733610	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	0.1082	0.0172	3.27E-10	0.0499	0.0363	1.70E-01	0.0765	0.0129	2.62E-09	0
rs28661692	3	104733669	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	-0.1088	0.0172	2.59E-10	-0.0511	0.0363	1.59E-01	-0.0765	0.0129	2.68E-09	0
rs16850766	3	104733714	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	-0.1083	0.0172	3.08E-10	-0.0499	0.0363	1.69E-01	-0.0763	0.0129	2.86E-09	0
rs28564343	3	104735374	24	104646815	104828166	T	G	0.1769	ALCAM	intergenic	0.1082	0.0172	3.16E-10	0.0489	0.0362	1.77E-01	0.0764	0.0129	2.84E-09	0
rs28421781	3	104735446	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	0.1093	0.0172	2.40E-10	0.0502	0.0362	1.65E-01	0.0769	0.0129	2.29E-09	0
rs28551708	3	104735633	24	104646815	104828166	T	G	0.1769	ALCAM	intergenic	-0.1122	0.0177	2.55E-10	-0.0492	0.0362	1.75E-01	-0.0838	0.0135	6.07E-10	0
rs28594489	3	104735634	24	104646815	104828166	T	C	0.1769	ALCAM	intergenic	-0.113	0.0178	2.12E-10	-0.0492	0.0362	1.75E-01	-0.0844	0.0136	5.46E-10	0
rs28423675	3	104735824	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	-0.1083	0.0172	3.06E-10	-0.0490	0.0362	1.76E-01	-0.0768	0.0129	2.26E-09	0
rs7646614	3	104736349	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	0.1085	0.0172	2.90E-10	0.0494	0.0363	1.73E-01	0.0769	0.0129	2.24E-09	0
rs6437554	3	104736464	24	104646815	104828166	A	G	0.1789	ALCAM	intergenic	0.1092	0.0172	2.25E-10	0.0504	0.0363	1.65E-01	0.0773	0.0129	1.78E-09	0
rs34360357	3	104736675	24	104646815	104828166	T	G	0.4135	ALCAM	intergenic	0.0877	0.0132	3.21E-11	0.0791	0.0277	4.28E-03	0.0516	0.0101	2.96E-07	1
rs17387070	3	104736772	24	104646815	104828166	A	G	0.4135	ALCAM	intergenic	-0.0878	0.0132	3.28E-11	-0.0798	0.0277	3.93E-03	-0.0522	0.0101	2.31E-07	1
rs6781572	3	104736846	24	104646815	104828166	A	G	0.1789	ALCAM	intergenic	-0.109	0.0172	2.40E-10	-0.0504	0.0363	1.65E-01	-0.0775	0.0129	1.64E-09	0
rs73852547	3	104737138	24	104646815	104828166	T	C	0.1769	ALCAM	intergenic	-0.1084	0.0172	3.06E-10	-0.0491	0.0363	1.76E-01	-0.0769	0.0129	2.24E-09	0
rs72989352	3	104737400	24	104646815	104828166	A	T	0.1769	ALCAM	intergenic	-0.1089	0.0172	2.54E-10	-0.0507	0.0363	1.63E-01	-0.0769	0.0129	2.25E-09	0
rs76481720	3	104737632	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	0.1086	0.0172	2.84E-10	0.0471	0.0363	1.95E-01	0.0768	0.0129	2.42E-09	0
rs60072080	3	104737669	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	-0.1084	0.0172	3.00E-10	-0.0494	0.0363	1.73E-01	-0.0770	0.0129	2.22E-09	0
rs58205062	3	104737769	24	104646815	104828166	T	G	0.1759	ALCAM	intergenic	0.1077	0.0172	3.87E-10	0.0510	0.0363	1.60E-01	0.0764	0.0129	2.94E-09	0
rs28735393	3	104738215	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	-0.1084	0.0172	3.08E-10	-0.0495	0.0363	1.73E-01	-0.0767	0.0129	2.52E-09	0
rs9857628	3	104738370	24	104646815	104828166	A	T	0.1769	ALCAM	intergenic	-0.1084	0.0172	3.08E-10	-0.0496	0.0363	1.72E-01	-0.0767	0.0129	2.52E-09	0
rs6437555	3	104738746	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	-0.1105	0.0173	1.59E-10	-0.0507	0.0365	1.65E-01	-0.0764	0.0129	2.88E-09	0
rs6437556	3	104738751	24	104646815	104828166	A	G	0.1769	ALCAM	intergenic	0.1111	0.0173	1.38E-10	0.0513	0.0365	1.60E-01	0.0766	0.0129	2.70E-09	0
rs9848945	3	104740628	24	104646815	104828166	T	G	0.173	ALCAM	intergenic	-0.1084	0.0172	3.09E-10	-0.0519	0.0364	1.54E-01	-0.0755	0.0129	4.36E-09	0
rs7626601	3	104742187	24	104646815	104828166	A	C	0.173	ALCAM	intergenic	-0.1083	0.0172	3.21E-10	-0.0520	0.0364	1.54E-01	-0.0757	0.0129	4.00E-09	0
rs9883825	3	104745091	24	104646815	104828166	A	G	0.4145	ALCAM	intergenic	-0.0881	0.0132	2.68E-11	-0.0770	0.0277	5.48E-03	-0.0508	0.0101	4.73E-07	1
rs9288797	3	104745255	24	104646815	104828166	A	G	0.173	ALCAM	intergenic	-0.1081	0.0172	3.73E-10	-0.0520	0.0364	1.53E-01	-0.0752	0.0129	5.50E-09	0
rs79873095	3	104745777	24	104646815	104828166	T	G	0.173	ALCAM	intergenic	-0.1081	0.0172	3.67E-10	-0.0530	0.0364	1.46E-01	-0.0751	0.0129	5.83E-09	0
rs9825019	3	104748374	24	104646815	104828166	A	G	0.4155	ALCAM	intergenic	-0.0876	0.0132	3.58E-11	-0.0758	0.0277	6.27E-03	-0.0493	0.0101	1.06E-06	1
rs7340550	3	104754015	24	104646815	104828166	T	G	0.173	ALCAM	intergenic	0.1066	0.0173	6.79E-10	0.0505	0.0362	1.64E-01	0.0751	0.0129	5.76E-09	0
rs13319556	3	104754543	24	104646815	104828166	A	T	0.174	ALCAM	intergenic	-0.1069	0.0173	6.20E-10	-0.0506	0.0362	1.63E-01	-0.0743	0.0129	8.19E-09	0
rs13325696	3	104755481	24	104646815	104828166	A	G	0.173	ALCAM	intergenic	-0.1068	0.0173	6.33E-10	-0.0502	0.0362	1.66E-01	-0.0744	0.0129	7.89E-09	0
rs9834649	3	104755849	24	104646815	104828166	A	C	0.2913	ALCAM	intergenic	-0.1119	0.0141	2.21E-15	-0.0945	0.0298	1.52E-03	-0.0659	0.0107	7.15E-10	1
rs1503079	3	104759032	24	104646815	104828166	T	C	0.4891	ALCAM	intergenic	0.0734	0.0129	1.35E-08	0.0679	0.0271	1.21E-02	0.0318	0.0099	1.30E-03	1
rs955251	3	104759845	24	104646815	104828166	A	C	0.4891	ALCAM	intergenic	-0.0734	0.0129	1.38E-08	-0.0668	0.0270	1.35E-02	-0.0320	0.0099	1.20E-03	1
rs955250	3	104759895	24	104646815	104828166	A	G	0.4891	ALCAM	intergenic	-0.0734	0.0129	1.34E-08	-0.0673	0.0270	1.29E-02	-0.0320	0.0099	1.19E-03	1
rs6800125	3	104760179	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0733	0.0129	1.41E-08	-0.0670	0.0270	1.33E-02	-0.0320	0.0099	1.18E-03	1
rs1566720	3	104761408	24	104646815	104828166	A	C	0.4891	ALCAM	intergenic	0.0734	0.0129	1.33E-08	0.0670	0.0270	1.32E-02	0.0321	0.0099	1.14E-03	1
rs1566719	3	104761448	24	104646815	104828166	A	T	0.4891	ALCAM	intergenic	-0.0735	0.0129	1.31E-08	-0.0669	0.0270	1.33E-02	NA	NA	NA	NA

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs1566718	3	104761637	24	104646815	104828166	A	G	0.4891	ALCAM	intergenic	0.0732	0.0129	1.54E-08	0.0669	0.0270	1.33E-02	0.0315	0.0099	1.45E-03	1
rs66833862	3	104762515	24	104646815	104828166	T	C	0.4901	ALCAM	intergenic	0.075	0.013	8.92E-09	0.0663	0.0270	1.42E-02	0.0331	0.0100	9.92E-04	1
rs12633310	3	104763667	24	104646815	104828166	A	G	0.4891	ALCAM	intergenic	0.0735	0.0129	1.30E-08	0.0661	0.0270	1.46E-02	0.0323	0.0099	1.09E-03	1
rs56169547	3	104764040	24	104646815	104828166	A	G	0.4891	ALCAM	intergenic	0.075	0.013	7.39E-09	0.0663	0.0270	1.42E-02	0.0321	0.0099	1.25E-03	1
rs35563949	3	104765663	24	104646815	104828166	A	T	0.4901	ALCAM	intergenic	0.0738	0.0129	1.13E-08	0.0679	0.0270	1.20E-02	NA	NA	NA	NA
rs4894900	3	104766656	24	104646815	104828166	A	G	0.4901	ALCAM	intergenic	-0.0736	0.0129	1.22E-08	-0.0675	0.0270	1.24E-02	-0.0325	0.0099	1.00E-03	1
rs1566716	3	104767455	24	104646815	104828166	T	C	0.4901	ALCAM	intergenic	-0.0741	0.0129	1.00E-08	-0.0677	0.0270	1.22E-02	-0.0325	0.0099	1.02E-03	1
rs1566717	3	104767509	24	104646815	104828166	A	T	0.4901	ALCAM	intergenic	-0.0741	0.0129	1.00E-08	-0.0676	0.0270	1.23E-02	NA	NA	NA	NA
rs953850	3	104767889	24	104646815	104828166	A	T	0.4881	ALCAM	intergenic	-0.0733	0.0129	1.45E-08	-0.0677	0.0270	1.22E-02	NA	NA	NA	NA
rs13090983	3	104768133	24	104646815	104828166	C	G	0.4881	ALCAM	intergenic	0.0733	0.0129	1.45E-08	0.0678	0.0270	1.21E-02	NA	NA	NA	NA
rs10933801	3	104769160	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0733	0.0129	1.42E-08	0.0677	0.0270	1.22E-02	0.0325	0.0099	1.01E-03	1
rs12633740	3	104769506	24	104646815	104828166	A	C	0.4881	ALCAM	intergenic	0.0746	0.013	9.61E-09	0.0678	0.0270	1.22E-02	0.0345	0.0100	5.39E-04	1
rs13059629	3	104769921	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0735	0.0129	1.29E-08	-0.0678	0.0270	1.20E-02	-0.0324	0.0099	1.02E-03	1
rs13060672	3	104770357	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0736	0.0129	1.28E-08	0.0678	0.0270	1.20E-02	0.0325	0.0099	1.01E-03	1
rs67773865	3	104770966	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0741	0.0129	1.03E-08	0.0679	0.0270	1.20E-02	0.0329	0.0099	8.75E-04	1
rs13066039	3	104771161	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.22E-08	-0.0683	0.0270	1.15E-02	-0.0325	0.0099	1.01E-03	1
rs13066506	3	104771184	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0738	0.0129	1.18E-08	0.0679	0.0270	1.20E-02	0.0325	0.0099	1.02E-03	1
rs35154832	3	104771559	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	-0.0738	0.0129	1.16E-08	-0.0688	0.0271	1.10E-02	-0.0324	0.0099	1.03E-03	1
rs34044731	3	104771580	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0738	0.0129	1.14E-08	0.0690	0.0270	1.08E-02	0.0325	0.0099	1.00E-03	1
rs1910328	3	104771826	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0733	0.0129	1.47E-08	0.0678	0.0270	1.21E-02	0.0326	0.0099	9.76E-04	1
rs1910329	3	104771860	24	104646815	104828166	C	G	0.4881	ALCAM	intergenic	0.0734	0.0129	1.35E-08	0.0679	0.0270	1.20E-02	NA	NA	NA	NA
rs35507961	3	104772393	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0735	0.0129	1.33E-08	0.0678	0.0270	1.21E-02	0.0324	0.0099	1.02E-03	1
rs35705376	3	104773479	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0735	0.0129	1.30E-08	-0.0670	0.0270	1.31E-02	-0.0324	0.0099	1.05E-03	1
rs12637494	3	104773965	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0735	0.0129	1.28E-08	0.0670	0.0270	1.31E-02	0.0326	0.0099	9.71E-04	1
rs10933802	3	104774304	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.19E-08	-0.0670	0.0270	1.31E-02	-0.0328	0.0099	9.15E-04	1
rs10804438	3	104774460	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0736	0.0129	1.23E-08	-0.0670	0.0270	1.31E-02	-0.0325	0.0099	1.00E-03	1
rs12163622	3	104774805	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0736	0.0129	1.25E-08	0.0667	0.0270	1.35E-02	0.0325	0.0099	9.88E-04	1
rs12163623	3	104774833	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	0.0737	0.0129	1.22E-08	0.0670	0.0270	1.31E-02	0.0325	0.0099	1.00E-03	1
rs10933803	3	104775181	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.23E-08	-0.0670	0.0270	1.31E-02	-0.0325	0.0099	1.01E-03	1
rs12639601	3	104775272	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0731	0.0129	1.63E-08	-0.0670	0.0270	1.31E-02	-0.0327	0.0099	9.58E-04	1
rs13064544	3	104776332	24	104646815	104828166	A	C	0.4881	ALCAM	intergenic	-0.0735	0.0129	1.31E-08	-0.0670	0.0270	1.31E-02	-0.0324	0.0099	1.03E-03	1
rs57241486	3	104776636	24	104646815	104828166	C	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.19E-08	-0.0670	0.0270	1.31E-02	NA	NA	NA	NA
rs6797909	3	104777026	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	0.0738	0.0129	1.18E-08	0.0670	0.0270	1.31E-02	0.0328	0.0099	9.16E-04	1
rs6798196	3	104777290	24	104646815	104828166	C	G	0.4881	ALCAM	intergenic	0.0736	0.0129	1.27E-08	0.0670	0.0270	1.31E-02	NA	NA	NA	NA
rs6798649	3	104777711	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	0.0735	0.0129	1.34E-08	0.0668	0.0270	1.35E-02	0.0327	0.0099	9.48E-04	1
rs10933804	3	104777958	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0739	0.0129	1.15E-08	-0.0658	0.0270	1.50E-02	-0.0329	0.0099	8.93E-04	1
rs10933805	3	104777973	24	104646815	104828166	C	G	0.4881	ALCAM	intergenic	-0.0739	0.0129	1.15E-08	-0.0658	0.0270	1.50E-02	NA	NA	NA	NA
rs11708913	3	104778145	24	104646815	104828166	A	T	0.4881	ALCAM	intergenic	-0.0739	0.0129	1.13E-08	-0.0666	0.0270	1.37E-02	NA	NA	NA	NA
rs11708967	3	104778270	24	104646815	104828166	A	C	0.4851	ALCAM	intergenic	-0.0803	0.0133	1.61E-09	-0.0667	0.0270	1.37E-02	-0.0410	0.0104	8.08E-05	1
rs34967119	3	104778430	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0765	0.0133	9.36E-09	0.0667	0.0270	1.36E-02	0.0342	0.0104	1.00E-03	1
rs2047806	3	104778810	24	104646815	104828166	A	C	0.4881	ALCAM	intergenic	0.0736	0.0129	1.30E-08	0.0679	0.0270	1.20E-02	0.0327	0.0099	9.47E-04	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs62260620	3	104779102	24	104646815	104828166	A	G	0.4851	ALCAM	intergenic	-0.0736	0.0129	1.29E-08	-0.0687	0.0270	1.10E-02	-0.0329	0.0099	8.73E-04	1
rs56146536	3	104779138	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0736	0.0129	1.29E-08	-0.0687	0.0270	1.10E-02	-0.0326	0.0099	9.74E-04	1
rs1032796	3	104779561	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0736	0.0129	1.28E-08	-0.0694	0.0270	1.02E-02	-0.0327	0.0099	9.44E-04	1
rs7651259	3	104779847	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0735	0.0129	1.36E-08	0.0699	0.0270	9.71E-03	0.0326	0.0099	9.70E-04	1
rs2399028	3	104779893	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0736	0.0129	1.26E-08	0.0694	0.0270	1.02E-02	0.0327	0.0099	9.39E-04	1
rs2134526	3	104780244	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0736	0.0129	1.28E-08	-0.0694	0.0270	1.02E-02	-0.0327	0.0099	9.30E-04	1
rs13073998	3	104780902	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0738	0.0129	1.16E-08	-0.0694	0.0270	1.02E-02	-0.0327	0.0099	9.37E-04	1
rs13095276	3	104781455	24	104646815	104828166	T	C	0.4861	ALCAM	intergenic	0.0739	0.0129	1.11E-08	0.0696	0.0270	9.94E-03	0.0329	0.0099	8.71E-04	1
rs9883267	3	104782005	24	104646815	104828166	T	C	0.4165	ALCAM	intergenic	-0.0841	0.0132	1.69E-10	-0.0702	0.0275	1.07E-02	-0.0486	0.0101	1.33E-06	1
rs6809713	3	104782428	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.20E-08	-0.0694	0.0270	1.02E-02	-0.0327	0.0099	9.17E-04	1
rs6800325	3	104783012	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0738	0.0129	1.16E-08	0.0695	0.0270	1.00E-02	0.0326	0.0099	9.55E-04	1
rs6800248	3	104783055	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0737	0.0129	1.18E-08	0.0695	0.0270	1.00E-02	0.0327	0.0099	9.35E-04	1
rs10933806	3	104783475	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	-0.0745	0.0129	8.51E-09	-0.0695	0.0270	1.00E-02	-0.0327	0.0099	9.26E-04	1
rs9814707	3	104783737	24	104646815	104828166	A	G	0.1779	ALCAM	intergenic	-0.1057	0.0172	7.23E-10	-0.0422	0.0362	2.44E-01	-0.0725	0.0128	1.68E-08	0
rs11706888	3	104783773	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0736	0.0129	1.27E-08	0.0696	0.0270	1.00E-02	0.0326	0.0099	9.68E-04	1
rs12635716	3	104784020	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.19E-08	-0.0695	0.0270	1.00E-02	-0.0326	0.0099	9.53E-04	1
rs10933807	3	104784330	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0743	0.0129	9.14E-09	0.0707	0.0270	8.84E-03	0.0326	0.0099	9.54E-04	1
rs6437560	3	104784922	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0738	0.0129	1.14E-08	-0.0702	0.0270	9.35E-03	-0.0326	0.0099	9.76E-04	1
rs7618073	3	104785204	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.21E-08	-0.0695	0.0270	1.01E-02	-0.0326	0.0099	9.68E-04	1
rs7650627	3	104785216	24	104646815	104828166	A	C	0.4881	ALCAM	intergenic	0.0738	0.0129	1.12E-08	0.0702	0.0270	9.30E-03	0.0326	0.0099	9.70E-04	1
rs7650875	3	104785261	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0737	0.0129	1.23E-08	0.0702	0.0270	9.33E-03	0.0328	0.0099	9.27E-04	1
rs7628576	3	104785371	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0738	0.0129	1.13E-08	-0.0702	0.0270	9.34E-03	-0.0326	0.0099	9.80E-04	1
rs1104503	3	104785888	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0738	0.0129	1.13E-08	-0.0702	0.0270	9.34E-03	-0.0325	0.0099	9.82E-04	1
rs1104502	3	104785935	24	104646815	104828166	T	C	0.4871	ALCAM	intergenic	0.0738	0.0129	1.13E-08	0.0702	0.0270	9.33E-03	0.0326	0.0099	9.66E-04	1
rs1587707	3	104786133	24	104646815	104828166	T	G	0.4891	ALCAM	intergenic	-0.0746	0.013	1.05E-08	-0.0680	0.0270	1.20E-02	-0.0330	0.0100	9.57E-04	1
rs2399027	3	104786221	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	0.0739	0.0129	1.12E-08	0.0702	0.0270	9.29E-03	0.0326	0.0099	9.74E-04	1
rs57951267	3	104786428	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0739	0.0129	1.12E-08	-0.0702	0.0270	9.29E-03	-0.0326	0.0099	9.74E-04	1
rs7609968	3	104786544	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	0.0739	0.0129	1.11E-08	0.0702	0.0270	9.37E-03	0.0326	0.0099	9.73E-04	1
rs2174113	3	104786848	24	104646815	104828166	A	C	0.4871	ALCAM	intergenic	-0.0738	0.0129	1.17E-08	-0.0675	0.0270	1.24E-02	-0.0326	0.0099	9.65E-04	1
rs2134527	3	104787185	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0738	0.0129	1.17E-08	-0.0675	0.0270	1.24E-02	-0.0326	0.0099	9.68E-04	1
rs2174114	3	104787255	24	104646815	104828166	A	C	0.4881	ALCAM	intergenic	0.0737	0.0129	1.25E-08	0.0675	0.0270	1.24E-02	0.0328	0.0099	9.14E-04	1
rs62258876	3	104787528	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0738	0.0129	1.17E-08	-0.0675	0.0270	1.24E-02	-0.0326	0.0099	9.68E-04	1
rs6437561	3	104788531	24	104646815	104828166	A	C	0.4881	ALCAM	intergenic	0.0738	0.0129	1.18E-08	0.0675	0.0270	1.24E-02	0.0326	0.0099	9.68E-04	1
rs2895296	3	104788762	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0742	0.0129	9.83E-09	-0.0674	0.0270	1.26E-02	-0.0326	0.0099	9.70E-04	1
rs2399026	3	104789107	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	0.0737	0.0129	1.23E-08	0.0676	0.0270	1.23E-02	0.0326	0.0099	9.71E-04	1
rs4522800	3	104789253	24	104646815	104828166	A	T	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.23E-08	-0.0676	0.0270	1.23E-02	NA	NA	NA	NA
rs4525898	3	104789294	24	104646815	104828166	A	C	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.23E-08	-0.0676	0.0270	1.23E-02	-0.0326	0.0099	9.69E-04	1
rs4276216	3	104789511	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0732	0.013	1.70E-08	0.0680	0.0270	1.19E-02	0.0326	0.0099	1.03E-03	1
rs4444734	3	104789572	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0737	0.0129	1.24E-08	0.0680	0.0270	1.18E-02	0.0323	0.0099	1.06E-03	1
rs62258878	3	104789859	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0753	0.0131	8.75E-09	-0.0680	0.0270	1.19E-02	-0.0335	0.0101	9.06E-04	1
rs17453821	3	104790120	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.24E-08	-0.0680	0.0270	1.19E-02	-0.0325	0.0099	1.00E-03	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs2399025	3	104790262	24	104646815	104828166	C	G	0.4881	ALCAM	intergenic	0.0737	0.0129	1.22E-08	0.0680	0.0270	1.19E-02	NA	NA	NA	NA
rs2895295	3	104790415	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.24E-08	-0.0680	0.0270	1.19E-02	-0.0326	0.0099	9.78E-04	1
rs12633839	3	104790781	24	104646815	104828166	T	C	0.4891	ALCAM	intergenic	-0.0744	0.0135	3.26E-08	-0.0659	0.0273	1.57E-02	-0.0362	0.0104	5.28E-04	1
rs2174117	3	104790914	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0751	0.0132	1.14E-08	0.0669	0.0271	1.34E-02	0.0335	0.0102	9.75E-04	1
rs2174116	3	104790927	24	104646815	104828166	C	G	0.4881	ALCAM	intergenic	0.0761	0.0131	6.88E-09	0.0669	0.0271	1.34E-02	NA	NA	NA	NA
rs2134542	3	104791106	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.22E-08	-0.0680	0.0270	1.19E-02	-0.0325	0.0099	9.97E-04	1
rs2134541	3	104791188	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.074	0.013	1.14E-08	-0.0680	0.0270	1.19E-02	-0.0329	0.0099	9.00E-04	1
rs12637068	3	104791391	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.25E-08	-0.0680	0.0270	1.19E-02	-0.0325	0.0099	1.00E-03	1
rs1503082	3	104791710	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.25E-08	-0.0680	0.0270	1.19E-02	-0.0325	0.0099	1.00E-03	1
rs1503083	3	104791792	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0738	0.0129	1.18E-08	-0.0680	0.0270	1.19E-02	-0.0325	0.0099	1.01E-03	1
rs1503084	3	104791812	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	0.0741	0.0129	1.05E-08	0.0679	0.0270	1.20E-02	0.0327	0.0099	9.30E-04	1
rs2202246	3	104792169	24	104646815	104828166	A	T	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.25E-08	-0.0680	0.0270	1.19E-02	NA	NA	NA	NA
rs12632482	3	104792646	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0736	0.0129	1.26E-08	0.0680	0.0270	1.18E-02	0.0325	0.0099	1.02E-03	1
rs12635443	3	104792828	24	104646815	104828166	T	G	0.4881	ALCAM	intergenic	-0.0736	0.0129	1.26E-08	-0.0680	0.0270	1.18E-02	-0.0324	0.0099	1.02E-03	1
rs12496781	3	104793180	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0737	0.0129	1.26E-08	-0.0680	0.0270	1.18E-02	-0.0324	0.0099	1.04E-03	1
rs4894903	3	104794115	24	104646815	104828166	A	T	0.4881	ALCAM	intergenic	0.0736	0.0129	1.29E-08	0.0680	0.0270	1.19E-02	NA	NA	NA	NA
rs7427968	3	104794254	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	0.0735	0.013	1.40E-08	0.0680	0.0270	1.19E-02	0.0326	0.0099	9.84E-04	1
rs1116674	3	104794380	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0736	0.0129	1.28E-08	-0.0680	0.0270	1.19E-02	-0.0322	0.0099	1.12E-03	1
rs10933808	3	104795049	24	104646815	104828166	T	C	0.4881	ALCAM	intergenic	-0.0735	0.0129	1.38E-08	-0.0680	0.0270	1.19E-02	-0.0322	0.0099	1.13E-03	1
rs12632078	3	104796874	24	104646815	104828166	T	C	0.493	ALCAM	intergenic	0.0766	0.013	3.48E-09	0.0695	0.0271	1.02E-02	0.0339	0.0099	6.30E-04	1
rs1587709	3	104796983	24	104646815	104828166	A	G	0.4861	ALCAM	intergenic	-0.0734	0.0129	1.45E-08	-0.0682	0.0270	1.17E-02	-0.0323	0.0099	1.07E-03	1
rs1587710	3	104797217	24	104646815	104828166	T	C	0.4861	ALCAM	intergenic	-0.0733	0.013	1.71E-08	-0.0682	0.0270	1.18E-02	-0.0322	0.0099	1.14E-03	1
rs1587716	3	104798102	24	104646815	104828166	T	G	0.493	ALCAM	intergenic	0.0764	0.013	4.41E-09	0.0703	0.0270	9.36E-03	0.0336	0.0099	7.05E-04	1
rs11715847	3	104798853	24	104646815	104828166	T	G	0.4861	ALCAM	intergenic	-0.073	0.013	1.97E-08	-0.0680	0.0271	1.20E-02	-0.0321	0.0099	1.20E-03	1
rs79553445	3	104799105	24	104646815	104828166	A	C	0.169	ALCAM	intergenic	0.1025	0.0176	5.15E-09	0.0477	0.0370	1.98E-01	0.0771	0.0132	5.37E-09	0
rs9809567	3	104799941	24	104646815	104828166	A	C	0.169	ALCAM	intergenic	0.1026	0.0176	5.06E-09	0.0475	0.0370	2.00E-01	0.0774	0.0132	4.63E-09	0
rs10933809	3	104800350	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0735	0.013	1.57E-08	0.0677	0.0271	1.24E-02	0.0319	0.0099	1.29E-03	1
rs6437565	3	104801746	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	-0.0732	0.013	1.81E-08	-0.0676	0.0271	1.25E-02	-0.0318	0.0099	1.33E-03	1
rs1503085	3	104802096	24	104646815	104828166	A	G	0.4881	ALCAM	intergenic	0.0731	0.013	1.90E-08	0.0667	0.0271	1.38E-02	0.0318	0.0099	1.31E-03	1
rs2654247	3	104805201	24	104646815	104828166	A	G	0.4602	ALCAM	intergenic	-0.0934	0.0131	9.66E-13	-0.0885	0.0272	1.13E-03	-0.0464	0.0099	3.07E-06	1
rs9881967	3	104821917	24	104646815	104828166	A	G	0.163	ALCAM	intergenic	-0.1099	0.0181	1.15E-09	-0.0352	0.0380	3.55E-01	-0.0774	0.0136	1.22E-08	0
rs2399023	3	104823350	24	104646815	104828166	A	G	0.3668	ALCAM	intergenic	0.0779	0.0136	9.74E-09	0.0584	0.0282	3.81E-02	0.0384	0.0103	2.04E-04	1
rs7615032	3	104828081	24	104646815	104828166	A	G	0.163	ALCAM	intergenic	-0.1118	0.0183	9.92E-10	-0.0413	0.0384	2.81E-01	-0.0747	0.0138	6.38E-08	0
rs153152	5	59842971	25	59823118	60465365	A	G	0.4076	PART1	ncRNA_exonic	0.0767	0.0134	1.12E-08	0.0857	0.0277	1.96E-03	0.0221	0.0103	3.11E-02	1
rs248912	5	59844079	25	59823118	60465365	T	C	0.4085	PART1	downstream	-0.0771	0.0134	9.17E-09	-0.0857	0.0277	1.95E-03	-0.0220	0.0102	3.18E-02	1
rs249070	5	59851527	25	59823118	60465365	T	C	0.4085	PART1	intergenic	0.0767	0.0133	9.06E-09	0.0829	0.0275	2.59E-03	0.0207	0.0103	4.36E-02	1
rs633628	5	59852636	25	59823118	60465365	T	C	0.4085	PART1	intergenic	-0.0769	0.0133	7.79E-09	-0.0829	0.0275	2.59E-03	-0.0218	0.0102	3.24E-02	1
rs60148983	5	59855032	25	59823118	60465365	C	G	0.4085	PART1	intergenic	-0.0773	0.0134	8.25E-09	-0.0828	0.0275	2.62E-03	-0.0207	0.0103	4.54E-02	1
rs3958943	5	59876749	25	59823118	60465365	T	C	0.4085	DEPDC1B	intergenic	-0.0762	0.0132	8.71E-09	-0.0843	0.0275	2.20E-03	-0.0211	0.0101	3.66E-02	1
rs55768631	5	59877191	25	59823118	60465365	A	T	0.4085	DEPDC1B	intergenic	0.0759	0.0133	1.02E-08	0.0836	0.0275	2.39E-03	0.0207	0.0101	4.03E-02	1
rs56166952	5	59906395	25	59823118	60465365	T	C	0.4085	DEPDC1B	intronic	0.0764	0.0132	7.04E-09	0.0832	0.0274	2.44E-03	0.0208	0.0101	3.87E-02	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs11951503	5	59918840	25	59823118	60465365	A	G	0.4085	DEPDC1B	intronic	0.0767	0.0132	6.35E-09	0.0819	0.0274	2.85E-03	0.0207	0.0101	3.99E-02	1
rs10939855	5	59930271	25	59823118	60465365	A	G	0.4215	DEPDC1B	intronic	-0.0838	0.0135	5.62E-10	-0.0829	0.0275	2.57E-03	-0.0211	0.0105	4.47E-02	1
rs1379116	5	59942400	25	59823118	60465365	A	G	0.4085	DEPDC1B	intronic	-0.077	0.0132	5.47E-09	-0.0840	0.0274	2.20E-03	-0.0218	0.0101	3.11E-02	1
rs72755157	5	59947386	25	59823118	60465365	A	C	0.4095	DEPDC1B	intronic	0.0811	0.0135	1.98E-09	0.0849	0.0274	1.95E-03	0.0203	0.0104	5.20E-02	0
rs4504343	5	59948395	25	59823118	60465365	C	G	0.4205	DEPDC1B	intronic	0.0764	0.0132	7.57E-09	0.0884	0.0274	1.27E-03	NA	NA	NA	NA
rs56347749	5	59951824	25	59823118	60465365	A	G	0.4205	DEPDC1B	intronic	0.0761	0.0132	8.78E-09	0.0888	0.0274	1.21E-03	0.0219	0.0102	3.14E-02	1
rs2198865	5	59954057	25	59823118	60465365	T	C	0.4095	DEPDC1B	intronic	-0.0754	0.0132	1.14E-08	-0.0858	0.0274	1.73E-03	-0.0210	0.0101	3.84E-02	1
rs59155887	5	59961543	25	59823118	60465365	A	G	0.4095	DEPDC1B	intronic	-0.0756	0.0132	1.07E-08	-0.0858	0.0274	1.73E-03	-0.0208	0.0101	4.02E-02	1
rs17387940	5	59967716	25	59823118	60465365	A	C	0.4095	DEPDC1B	intronic	0.074	0.0132	1.89E-08	0.0860	0.0274	1.69E-03	0.0214	0.0100	3.23E-02	1
rs12517174	5	59969015	25	59823118	60465365	T	C	0.4095	DEPDC1B	intronic	0.074	0.0132	1.86E-08	0.0860	0.0274	1.69E-03	0.0214	0.0100	3.23E-02	1
rs56726435	5	59975064	25	59823118	60465365	T	C	0.4095	DEPDC1B	intronic	0.0743	0.0132	1.63E-08	0.0853	0.0274	1.86E-03	0.0214	0.0100	3.26E-02	1
rs11741754	5	59977058	25	59823118	60465365	A	G	0.4095	DEPDC1B	intronic	-0.0746	0.0132	1.46E-08	-0.0851	0.0274	1.89E-03	-0.0213	0.0100	3.33E-02	1
rs11955398	5	59981085	25	59823118	60465365	A	C	0.4095	DEPDC1B	intronic	-0.0745	0.0132	1.51E-08	-0.0847	0.0274	2.00E-03	-0.0213	0.0100	3.31E-02	1
rs10939858	5	59983481	25	59823118	60465365	A	T	0.4095	DEPDC1B	intronic	-0.0766	0.0135	1.38E-08	-0.0849	0.0274	1.95E-03	-0.0211	0.0105	4.46E-02	1
rs7704338	5	59986155	25	59823118	60465365	T	C	0.4553	DEPDC1B	intronic	-0.0748	0.013	9.28E-09	-0.0752	0.0270	5.39E-03	-0.0218	0.0100	2.90E-02	1
rs7719611	5	59988547	25	59823118	60465365	A	G	0.4553	DEPDC1B	intronic	-0.0746	0.013	1.03E-08	-0.0748	0.0270	5.68E-03	-0.0217	0.0100	2.94E-02	1
rs12517207	5	59993268	25	59823118	60465365	T	C	0.4095	DEPDC1B	intronic	0.0745	0.0132	1.56E-08	0.0860	0.0274	1.71E-03	0.0211	0.0100	3.53E-02	1
rs716344	5	60012521	25	59823118	60465365	C	G	0.4066	DEPDC1B	intergenic	-0.0799	0.0132	1.27E-09	-0.0753	0.0274	5.98E-03	-0.0214	0.0101	3.38E-02	1
rs7709056	5	60024091	25	59823118	60465365	A	G	0.4076	KRT8P31	intergenic	-0.0796	0.0133	2.10E-09	-0.0736	0.0274	7.20E-03	-0.0199	0.0103	5.23E-02	0
rs7381195	5	60030791	25	59823118	60465365	A	T	0.3638	KRT8P31	intergenic	0.0866	0.014	5.27E-10	0.0750	0.0279	7.13E-03	0.0221	0.0107	4.00E-02	1
rs7720233	5	60046832	25	59823118	60465365	T	C	0.4085	ELOVL7	downstream	0.0763	0.0131	6.37E-09	0.0713	0.0274	9.23E-03	0.0232	0.0101	2.13E-02	1
rs10043291	5	60058858	25	59823118	60465365	T	C	0.4095	ELOVL7	intronic	0.0761	0.0131	6.96E-09	0.0716	0.0274	8.98E-03	0.0233	0.0100	2.03E-02	1
rs4527549	5	60062745	25	59823118	60465365	T	C	0.4095	ELOVL7	intronic	-0.0768	0.0131	4.93E-09	-0.0730	0.0274	7.79E-03	-0.0233	0.0100	2.03E-02	1
rs1460958	5	60063576	25	59823118	60465365	A	G	0.4105	ELOVL7	intronic	0.0766	0.0131	5.45E-09	0.0724	0.0274	8.25E-03	0.0231	0.0100	2.15E-02	1
rs1444237	5	60063953	25	59823118	60465365	T	C	0.4085	ELOVL7	intronic	0.0767	0.0131	5.17E-09	0.0715	0.0274	9.05E-03	0.0226	0.0100	2.44E-02	1
rs13158665	5	60069057	25	59823118	60465365	T	C	0.4394	ELOVL7	intronic	0.0779	0.0132	3.20E-09	0.0820	0.0271	2.47E-03	0.0213	0.0101	3.56E-02	1
rs1444240	5	60069934	25	59823118	60465365	A	G	0.4264	ELOVL7	intronic	0.079	0.0132	2.13E-09	0.0753	0.0273	5.86E-03	0.0233	0.0102	2.18E-02	1
rs6874699	5	60074000	25	59823118	60465365	T	C	0.4254	ELOVL7	intronic	-0.0788	0.0132	2.33E-09	-0.0738	0.0273	6.91E-03	-0.0236	0.0102	2.02E-02	1
rs4353980	5	60075328	25	59823118	60465365	T	C	0.4264	ELOVL7	intronic	0.0787	0.0132	2.42E-09	0.0736	0.0273	7.04E-03	0.0236	0.0102	2.04E-02	1
rs10068474	5	60077912	25	59823118	60465365	T	G	0.4254	ELOVL7	intronic	-0.0784	0.0132	2.72E-09	-0.0737	0.0273	6.95E-03	-0.0236	0.0102	2.06E-02	1
rs10062240	5	60078412	25	59823118	60465365	T	C	0.4254	ELOVL7	intronic	0.0785	0.0132	2.67E-09	0.0737	0.0273	6.95E-03	0.0242	0.0102	1.72E-02	1
rs4700391	5	60082641	25	59823118	60465365	T	C	0.4264	ELOVL7	intronic	-0.0821	0.0138	2.89E-09	-0.0725	0.0273	7.98E-03	-0.0186	0.0108	8.55E-02	0
rs10072745	5	60083275	25	59823118	60465365	A	C	0.4642	ELOVL7	UTR5	-0.0732	0.0131	2.20E-08	-0.0961	0.0271	4.03E-04	-0.0251	0.0100	1.25E-02	1
rs6449500	5	60083903	25	59823118	60465365	A	G	0.4642	ELOVL7	intronic	0.0731	0.0131	2.29E-08	0.0968	0.0271	3.67E-04	0.0252	0.0100	1.21E-02	1
rs1870015	5	60085763	25	59823118	60465365	A	G	0.4642	ELOVL7	intronic	-0.0729	0.0131	2.57E-08	-0.0968	0.0271	3.65E-04	-0.0240	0.0101	1.71E-02	1
rs12519587	5	60086900	25	59823118	60465365	T	C	0.4284	ELOVL7	intronic	-0.0771	0.0132	5.15E-09	-0.0857	0.0273	1.70E-03	-0.0226	0.0101	2.50E-02	1
rs6872863	5	60088148	25	59823118	60465365	A	G	0.4672	ELOVL7	intronic	0.0724	0.013	2.57E-08	0.0968	0.0271	3.64E-04	0.0238	0.0099	1.62E-02	1
rs6873181	5	60088250	25	59823118	60465365	T	C	0.4672	ELOVL7	intronic	-0.0724	0.013	2.55E-08	-0.0968	0.0271	3.64E-04	-0.0238	0.0099	1.62E-02	1
rs6894672	5	60088255	25	59823118	60465365	T	C	0.4672	ELOVL7	intronic	0.0724	0.013	2.52E-08	0.0968	0.0271	3.64E-04	0.0238	0.0099	1.64E-02	1
rs10057395	5	60088794	25	59823118	60465365	A	G	0.4463	ELOVL7	intronic	0.0729	0.0131	2.61E-08	0.0835	0.0272	2.17E-03	0.0266	0.0100	8.14E-03	1
rs921897	5	60089137	25	59823118	60465365	A	G	0.4642	ELOVL7	intronic	-0.0734	0.013	1.67E-08	-0.0975	0.0271	3.32E-04	-0.0237	0.0099	1.66E-02	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs10076679	5	60090951	25	59823118	60465365	C	G	0.4642	ELOVL7	intronic	0.0736	0.013	1.52E-08	0.0950	0.0271	4.68E-04	NA	NA	NA	NA
rs10076742	5	60091046	25	59823118	60465365	T	C	0.4642	ELOVL7	intronic	-0.0738	0.013	1.40E-08	-0.0946	0.0271	4.95E-04	-0.0236	0.0099	1.69E-02	1
rs6890201	5	60091192	25	59823118	60465365	C	G	0.4642	ELOVL7	intronic	0.0738	0.013	1.40E-08	0.0946	0.0271	4.94E-04	NA	NA	NA	NA
rs6875456	5	60091330	25	59823118	60465365	T	C	0.4642	ELOVL7	intronic	0.0737	0.013	1.44E-08	0.0946	0.0271	4.94E-04	0.0236	0.0099	1.70E-02	1
rs6894750	5	60091556	25	59823118	60465365	A	G	0.4642	ELOVL7	intronic	0.0737	0.013	1.43E-08	0.0946	0.0271	4.95E-04	0.0235	0.0099	1.79E-02	1
rs6876335	5	60091818	25	59823118	60465365	T	C	0.4642	ELOVL7	intronic	0.0739	0.013	1.29E-08	0.0946	0.0271	4.95E-04	0.0235	0.0099	1.75E-02	1
rs6449501	5	60092687	25	59823118	60465365	A	G	0.4642	ELOVL7	intronic	-0.0739	0.013	1.33E-08	-0.0949	0.0271	4.75E-04	-0.0235	0.0099	1.75E-02	1
rs4235481	5	60093387	25	59823118	60465365	T	C	0.4642	ELOVL7	intronic	-0.0739	0.013	1.32E-08	-0.0951	0.0271	4.59E-04	-0.0235	0.0099	1.74E-02	1
rs4235482	5	60093612	25	59823118	60465365	A	G	0.4642	ELOVL7	intronic	0.0738	0.013	1.37E-08	0.0950	0.0271	4.69E-04	0.0235	0.0099	1.75E-02	1
rs57468227	5	60095004	25	59823118	60465365	T	C	0.3678	ELOVL7	intronic	0.0801	0.0137	5.45E-09	0.0841	0.0278	2.53E-03	0.0213	0.0106	4.36E-02	1
rs4482855	5	60096497	25	59823118	60465365	T	C	0.4652	ELOVL7	intronic	0.0726	0.013	2.45E-08	0.0953	0.0272	4.57E-04	0.0236	0.0099	1.73E-02	1
rs4700393	5	60098267	25	59823118	60465365	A	G	0.4602	ELOVL7	intronic	0.0733	0.013	1.79E-08	0.0993	0.0272	2.56E-04	0.0238	0.0099	1.66E-02	1
rs10077663	5	60103492	25	59823118	60465365	A	G	0.4652	ELOVL7	intronic	0.0719	0.013	3.27E-08	0.0955	0.0272	4.40E-04	0.0238	0.0099	1.64E-02	1
rs61160187	5	60111579	25	59823118	60465365	A	G	0.3678	ELOVL7	intronic	0.0797	0.0138	7.04E-09	0.0834	0.0278	2.75E-03	0.0224	0.0106	3.39E-02	1
rs4700394	5	60117202	25	59823118	60465365	A	T	0.4642	ELOVL7	intronic	0.0711	0.013	4.74E-08	0.0906	0.0271	8.43E-04	NA	NA	NA	NA
rs6893642	5	60117723	25	59823118	60465365	T	C	0.4642	ELOVL7	intronic	0.0714	0.013	4.24E-08	0.0898	0.0271	9.38E-04	0.0260	0.0099	8.89E-03	1
rs1445293	5	60119737	25	59823118	60465365	A	G	0.4642	ELOVL7	intronic	0.0713	0.013	4.57E-08	0.0906	0.0271	8.49E-04	0.0259	0.0099	9.06E-03	1
rs1807017	5	60127724	25	59823118	60465365	T	C	0.4254	ELOVL7	intronic	0.0788	0.0132	2.44E-09	0.0846	0.0274	2.05E-03	0.0261	0.0101	9.80E-03	1
rs62372102	5	60139881	25	59823118	60465365	A	G	0.4553	ELOVL7	intronic	0.0796	0.0131	1.43E-09	0.0792	0.0272	3.57E-03	0.0249	0.0101	1.35E-02	1
rs12654306	5	60184856	25	59823118	60465365	A	C	0.4275	ERCC8	intronic	0.074	0.0133	2.94E-08	0.0872	0.0276	1.60E-03	0.0308	0.0103	2.67E-03	1
rs7722373	5	60247815	25	59823118	60465365	A	G	0.4612	NDUFAF2	intronic	-0.079	0.0131	1.61E-09	-0.0816	0.0272	2.67E-03	-0.0299	0.0101	3.17E-03	1
rs17419290	5	60307904	25	59823118	60465365	A	G	0.4056	NDUFAF2	intronic	0.0731	0.0133	4.15E-08	0.0909	0.0275	9.29E-04	0.0363	0.0102	3.71E-04	1
rs10939879	5	60315823	25	59823118	60465365	T	C	0.4135	NDUFAF2	intronic	0.0727	0.0133	4.12E-08	0.0973	0.0274	3.80E-04	0.0395	0.0101	9.14E-05	1
rs76470478	6	126613946	26	126525715	127369230	T	C	0.02783	PPP1R14BP5	intergenic	-0.2206	0.0373	3.43E-09	-0.1571	0.0726	3.05E-02	-0.2034	0.0301	1.36E-11	1
rs117892760	6	126666648	26	126525715	127369230	T	C	0.02386	CENPW	intronic	-0.2224	0.0391	1.27E-08	-0.2087	0.0741	4.85E-03	-0.2376	0.0335	1.29E-12	1
rs1578060	6	126712247	26	126525715	127369230	C	G	0.4533	CENPW	intergenic	-0.0744	0.0131	1.37E-08	-0.0805	0.0273	3.21E-03	NA	NA	NA	NA
rs1591805	6	126717064	26	126525715	127369230	A	G	0.4911	CENPW	intergenic	0.0793	0.0132	2.01E-09	0.0763	0.0271	4.92E-03	0.0532	0.0102	2.06E-07	1
rs9398805	6	126726295	26	126525715	127369230	T	C	0.4543	CENPW	intergenic	-0.0749	0.0131	1.04E-08	-0.0772	0.0273	4.69E-03	-0.0550	0.0100	3.63E-08	1
rs4897179	6	126727930	26	126525715	127369230	A	G	0.4543	CENPW	intergenic	-0.0785	0.0133	3.29E-09	-0.0774	0.0273	4.62E-03	-0.0592	0.0102	6.23E-09	1
rs4897180	6	126727950	26	126525715	127369230	A	T	0.4543	CENPW	intergenic	0.0751	0.0132	1.19E-08	0.0776	0.0273	4.51E-03	NA	NA	NA	NA
rs75343521	6	126732511	26	126525715	127369230	T	C	0.02684	CENPW	intergenic	-0.2458	0.0373	4.25E-11	-0.1573	0.0702	2.50E-02	-0.1964	0.0308	1.93E-10	1
rs9321065	6	126744087	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	-0.0754	0.0131	8.62E-09	-0.0776	0.0273	4.49E-03	-0.0552	0.0100	3.42E-08	1
rs2039735	6	126745076	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	0.0785	0.0132	3.11E-09	0.0779	0.0273	4.35E-03	0.0578	0.0102	1.27E-08	1
rs139214174	6	126745633	26	126525715	127369230	A	C	0.02684	MIR588	intergenic	-0.2502	0.0375	2.38E-11	-0.1568	0.0708	2.67E-02	-0.2022	0.0313	1.12E-10	1
rs1538172	6	126748493	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	0.0757	0.0131	7.24E-09	0.0794	0.0273	3.65E-03	0.0550	0.0100	3.59E-08	1
rs9401881	6	126751921	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.0755	0.0131	7.95E-09	-0.0774	0.0273	4.59E-03	-0.0550	0.0100	3.53E-08	1
rs4565329	6	126752798	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.0752	0.0131	9.15E-09	-0.0773	0.0273	4.66E-03	-0.0550	0.0100	3.52E-08	1
rs1538170	6	126752874	26	126525715	127369230	T	C	0.4563	MIR588	intergenic	-0.0755	0.0131	7.69E-09	-0.0773	0.0273	4.66E-03	-0.0550	0.0100	3.54E-08	1
rs1538171	6	126752884	26	126525715	127369230	C	G	0.4563	MIR588	intergenic	0.0754	0.0131	8.26E-09	0.0773	0.0273	4.66E-03	NA	NA	NA	NA
rs4897181	6	126753564	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.0758	0.0131	6.96E-09	-0.0773	0.0273	4.62E-03	-0.0550	0.0100	3.51E-08	1
rs9401882	6	126755055	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	0.0759	0.0131	6.70E-09	0.0773	0.0273	4.65E-03	0.0550	0.0100	3.69E-08	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs4897182	6	126755642	26	126525715	127369230	T	G	0.4553	MIR588	intergenic	0.076	0.0131	6.33E-09	0.0772	0.0273	4.70E-03	0.0547	0.0100	4.18E-08	1
rs9375439	6	126758540	26	126525715	127369230	C	G	0.4543	MIR588	intergenic	0.076	0.0131	6.19E-09	0.0774	0.0273	4.58E-03	NA	NA	NA	NA
rs9398808	6	126758791	26	126525715	127369230	T	G	0.4543	MIR588	intergenic	-0.0758	0.0131	6.65E-09	-0.0774	0.0273	4.58E-03	-0.0550	0.0100	3.66E-08	1
rs9385399	6	126759033	26	126525715	127369230	T	G	0.4543	MIR588	intergenic	-0.0758	0.0131	6.89E-09	-0.0769	0.0273	4.87E-03	-0.0550	0.0100	3.64E-08	1
rs1415671	6	126759587	26	126525715	127369230	T	G	0.4543	MIR588	intergenic	0.0759	0.0131	6.40E-09	0.0771	0.0273	4.73E-03	0.0550	0.0100	3.60E-08	1
rs2184968	6	126760994	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	0.0748	0.0131	1.13E-08	0.0778	0.0273	4.44E-03	0.0553	0.0100	3.18E-08	1
rs2152876	6	126761228	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	-0.0757	0.0131	7.17E-09	-0.0780	0.0273	4.26E-03	-0.0550	0.0100	3.78E-08	1
rs9385400	6	126764190	26	126525715	127369230	T	G	0.4543	MIR588	intergenic	0.0758	0.0131	6.96E-09	0.0773	0.0273	4.62E-03	0.0547	0.0100	4.34E-08	1
rs1361107	6	126767511	26	126525715	127369230	A	C	0.4583	MIR588	intergenic	0.0758	0.0131	7.23E-09	0.0764	0.0273	5.18E-03	0.0549	0.0100	4.14E-08	1
rs1361108	6	126767600	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.0761	0.0131	5.93E-09	-0.0772	0.0273	4.68E-03	-0.0549	0.0100	4.03E-08	1
rs1337735	6	126771024	26	126525715	127369230	A	T	0.4543	MIR588	intergenic	-0.0753	0.0131	8.87E-09	-0.0776	0.0273	4.48E-03	NA	NA	NA	NA
rs1361109	6	126771143	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.0759	0.0131	6.77E-09	-0.0776	0.0273	4.46E-03	-0.0551	0.0100	3.54E-08	1
rs1572569	6	126771687	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	-0.0758	0.0131	7.11E-09	-0.0778	0.0273	4.37E-03	-0.0549	0.0100	3.94E-08	1
rs2184967	6	126773487	26	126525715	127369230	T	C	0.4533	MIR588	intergenic	-0.0749	0.0131	1.05E-08	-0.0779	0.0273	4.33E-03	-0.0548	0.0100	4.37E-08	1
rs4559102	6	126773580	26	126525715	127369230	A	G	0.4533	MIR588	intergenic	-0.0752	0.0131	9.05E-09	-0.0784	0.0273	4.06E-03	-0.0548	0.0100	4.30E-08	1
rs9388494	6	126776094	26	126525715	127369230	T	G	0.4543	MIR588	intergenic	-0.074	0.0131	1.62E-08	-0.0780	0.0273	4.27E-03	-0.0540	0.0100	7.39E-08	1
rs9375441	6	126778600	26	126525715	127369230	A	G	0.4533	MIR588	intergenic	-0.0754	0.0131	8.36E-09	-0.0786	0.0273	3.99E-03	-0.0547	0.0100	4.52E-08	1
rs4895808	6	126781434	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.0752	0.0131	9.47E-09	-0.0779	0.0273	4.30E-03	-0.0547	0.0100	4.45E-08	1
rs9388495	6	126782457	26	126525715	127369230	A	G	0.4553	MIR588	intergenic	-0.0756	0.0131	7.92E-09	-0.0784	0.0273	4.06E-03	-0.0546	0.0100	4.97E-08	1
rs9388496	6	126785062	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	0.0752	0.0131	9.24E-09	0.0776	0.0273	4.43E-03	0.0543	0.0100	5.65E-08	1
rs1844594	6	126788107	26	126525715	127369230	A	G	0.4553	MIR588	intergenic	-0.0755	0.0131	8.19E-09	-0.0779	0.0273	4.30E-03	-0.0542	0.0100	6.26E-08	1
rs9398809	6	126789144	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.0755	0.0131	8.11E-09	-0.0779	0.0273	4.30E-03	-0.0543	0.0100	5.55E-08	1
rs9385401	6	126789472	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.075	0.0131	1.01E-08	-0.0779	0.0273	4.30E-03	-0.0542	0.0100	5.85E-08	1
rs9401883	6	126797111	26	126525715	127369230	A	G	0.4553	MIR588	intergenic	0.0749	0.0131	1.05E-08	0.0782	0.0273	4.17E-03	0.0543	0.0100	5.43E-08	1
rs1159619	6	126801144	26	126525715	127369230	A	C	0.4543	MIR588	intergenic	-0.0744	0.0131	1.33E-08	-0.0788	0.0273	3.98E-03	-0.0541	0.0100	6.15E-08	1
rs9375442	6	126803137	26	126525715	127369230	A	C	0.4543	MIR588	intergenic	0.076	0.0131	6.69E-09	0.0778	0.0273	4.35E-03	0.0550	0.0100	3.92E-08	1
rs2050644	6	126805255	26	126525715	127369230	A	G	0.4543	MIR588	upstream	0.0747	0.0131	1.15E-08	0.0781	0.0273	4.23E-03	0.0541	0.0100	5.99E-08	1
rs4422634	6	126806676	26	126525715	127369230	T	C	0.4543	MIR588	downstream	0.0751	0.0131	9.54E-09	0.0786	0.0273	3.95E-03	0.0535	0.0100	8.37E-08	1
rs1120786	6	126808637	26	126525715	127369230	T	G	0.4543	MIR588	intergenic	0.0745	0.0131	1.32E-08	0.0786	0.0273	3.98E-03	0.0544	0.0100	5.77E-08	1
rs9372839	6	126809870	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	-0.0747	0.0131	1.14E-08	-0.0788	0.0273	3.90E-03	-0.0545	0.0100	5.09E-08	1
rs2326451	6	126811928	26	126525715	127369230	A	T	0.4533	MIR588	intergenic	0.0747	0.0131	1.18E-08	0.0765	0.0273	5.14E-03	NA	NA	NA	NA
rs9398810	6	126815604	26	126525715	127369230	A	C	0.4543	MIR588	intergenic	-0.0748	0.0131	1.09E-08	-0.0784	0.0273	4.09E-03	-0.0544	0.0100	5.21E-08	1
rs4418209	6	126819699	26	126525715	127369230	T	G	0.4543	MIR588	intergenic	0.0748	0.0131	1.08E-08	0.0790	0.0273	3.81E-03	0.0544	0.0100	5.10E-08	1
rs9372840	6	126822635	26	126525715	127369230	A	C	0.4543	MIR588	intergenic	0.0755	0.0131	7.97E-09	0.0799	0.0273	3.41E-03	0.0549	0.0100	4.15E-08	1
rs9401885	6	126825837	26	126525715	127369230	C	G	0.4543	MIR588	intergenic	0.075	0.0131	9.80E-09	0.0800	0.0273	3.36E-03	NA	NA	NA	NA
rs2130603	6	126826819	26	126525715	127369230	A	C	0.4543	MIR588	intergenic	0.075	0.0131	1.04E-08	0.0799	0.0273	3.40E-03	0.0553	0.0100	3.50E-08	1
rs7738135	6	126829981	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	-0.0749	0.0131	1.05E-08	-0.0800	0.0273	3.35E-03	-0.0550	0.0100	4.29E-08	1
rs4053271	6	126830512	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	0.0748	0.0131	1.12E-08	0.0800	0.0273	3.35E-03	0.0551	0.0100	4.08E-08	1
rs1490387	6	126834083	26	126525715	127369230	A	C	0.4543	MIR588	intergenic	-0.0751	0.0131	9.48E-09	-0.0801	0.0273	3.35E-03	-0.0551	0.0100	3.80E-08	1
rs9375446	6	126835015	26	126525715	127369230	A	G	0.4543	MIR588	intergenic	-0.075	0.0131	9.61E-09	-0.0800	0.0273	3.35E-03	-0.0551	0.0100	3.83E-08	1
rs1490388	6	126835655	26	126525715	127369230	T	C	0.4543	MIR588	intergenic	-0.075	0.0131	9.76E-09	-0.0803	0.0273	3.27E-03	-0.0551	0.0100	3.78E-08	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs1907067	6	126837663	26	126525715	127369230	A	C	0.4543	MIR588	intergenic	0.0749	0.0131	1.05E-08	0.0806	0.0273	3.15E-03	0.0551	0.0100	3.74E-08	1
rs1602278	6	126838605	26	126525715	127369230	A	C	0.4553	MIR588	intergenic	0.0754	0.0131	8.34E-09	0.0809	0.0273	3.05E-03	0.0552	0.0100	3.73E-08	1
rs1337736	6	126845380	26	126525715	127369230	A	G	0.1998	MIR588	intergenic	-0.1244	0.0164	3.40E-14	-0.1115	0.0328	6.78E-04	-0.0822	0.0126	6.62E-11	1
rs9375447	6	126874091	26	126525715	127369230	A	G	0.4821	RNU6-200P	intergenic	0.071	0.013	4.53E-08	0.0813	0.0272	2.79E-03	0.0563	0.0100	1.54E-08	1
rs1490385	6	126875521	26	126525715	127369230	T	C	0.4821	RNU6-200P	intergenic	-0.0712	0.013	4.35E-08	-0.0820	0.0272	2.56E-03	-0.0561	0.0100	2.10E-08	1
rs9401890	6	126881295	26	126525715	127369230	A	G	0.4831	RNU6-200P	intergenic	0.0718	0.013	3.72E-08	0.0815	0.0272	2.72E-03	0.0565	0.0101	2.08E-08	1
rs9401891	6	126894135	26	126525715	127369230	T	G	0.4811	RNU6-200P	intergenic	-0.0724	0.013	2.76E-08	-0.0827	0.0272	2.38E-03	-0.0577	0.0100	8.20E-09	1
rs9401892	6	126895368	26	126525715	127369230	A	G	0.4811	RNU6-200P	intergenic	-0.0708	0.013	4.90E-08	-0.0832	0.0272	2.22E-03	-0.0555	0.0099	2.34E-08	1
rs4621655	6	126896107	26	126525715	127369230	A	G	0.4811	RNU6-200P	intergenic	-0.0712	0.013	4.21E-08	-0.0832	0.0272	2.22E-03	-0.0556	0.0099	2.32E-08	1
rs4621656	6	126896168	26	126525715	127369230	C	G	0.4811	RNU6-200P	intergenic	-0.0709	0.013	4.66E-08	-0.0832	0.0272	2.20E-03	NA	NA	NA	NA
rs4621657	6	126896227	26	126525715	127369230	A	G	0.4811	RNU6-200P	intergenic	-0.0711	0.013	4.33E-08	-0.0832	0.0272	2.22E-03	-0.0556	0.0099	2.29E-08	1
rs1844593	6	126897827	26	126525715	127369230	A	G	0.4821	RNU6-200P	intergenic	-0.0713	0.013	3.96E-08	-0.0832	0.0272	2.22E-03	-0.0553	0.0100	2.76E-08	1
rs3861455	6	126897969	26	126525715	127369230	A	C	0.4811	RNU6-200P	intergenic	0.0711	0.013	4.35E-08	0.0832	0.0272	2.21E-03	0.0554	0.0099	2.52E-08	1
rs3861457	6	126902245	26	126525715	127369230	T	C	0.4821	RNU6-200P	intergenic	0.0717	0.013	3.36E-08	0.0832	0.0272	2.22E-03	0.0551	0.0100	3.13E-08	1
rs9388501	6	126903011	26	126525715	127369230	T	C	0.4811	RNU6-200P	intergenic	0.072	0.013	3.00E-08	0.0832	0.0272	2.21E-03	0.0549	0.0100	3.38E-08	1
rs4427021	6	126938446	26	126525715	127369230	T	C	0.1998	VIMP1	intergenic	-0.1219	0.0161	3.64E-14	-0.1114	0.0327	6.48E-04	-0.0796	0.0124	1.24E-10	1
rs6569466	6	126961319	26	126525715	127369230	T	C	0.2008	PRELID1P1	intergenic	-0.1202	0.0159	3.92E-14	-0.1149	0.0326	4.29E-04	-0.0800	0.0122	5.65E-11	1
rs74580701	6	127000881	26	126525715	127369230	A	G	0.02684	RPS4XP9	intergenic	0.2316	0.0382	1.30E-09	0.1248	0.0683	6.75E-02	0.2288	0.0361	2.34E-10	0
rs9375452	6	127014862	26	126525715	127369230	T	C	0.2028	RPS4XP9	intergenic	-0.1227	0.0159	1.09E-14	-0.1145	0.0326	4.41E-04	-0.0803	0.0122	4.05E-11	1
rs853983	6	127046153	26	126525715	127369230	A	G	0.4901	RPS4XP9	intergenic	0.0712	0.013	4.46E-08	0.0730	0.0272	7.24E-03	0.0590	0.0100	4.29E-09	1
rs1262555	6	127052816	26	126525715	127369230	A	G	0.4911	RPS4XP9	intergenic	0.0742	0.0132	2.16E-08	0.0735	0.0272	6.91E-03	0.0600	0.0104	7.55E-09	1
rs190958130	6	127052822	26	126525715	127369230	C	G	0.02684	RPS4XP9	intergenic	0.2397	0.0391	8.47E-10	0.1569	0.0718	2.89E-02	0.2119	0.0368	8.66E-09	1
rs9401903	6	127055771	26	126525715	127369230	T	C	0.2137	RPS4XP9	intergenic	-0.1227	0.0156	4.31E-15	-0.0999	0.0322	1.91E-03	-0.0821	0.0120	8.13E-12	1
rs79636188	6	127078181	26	126525715	127369230	T	C	0.02684	RPS4XP9	intergenic	0.2358	0.0385	8.67E-10	0.1417	0.0697	4.21E-02	0.2069	0.0370	2.18E-08	1
rs1262551	6	127078211	26	126525715	127369230	T	C	0.4901	RPS4XP9	intergenic	0.0714	0.0131	4.78E-08	0.0728	0.0272	7.46E-03	0.0627	0.0102	7.41E-10	1
rs1262552	6	127078752	26	126525715	127369230	T	C	0.4911	RPS4XP9	intergenic	0.0714	0.0131	4.83E-08	0.0722	0.0272	7.94E-03	0.0628	0.0102	6.98E-10	1
rs1343222	6	127081190	26	126525715	127369230	T	C	0.2147	RPS4XP9	intergenic	0.1214	0.0155	4.24E-15	0.0975	0.0321	2.43E-03	0.0802	0.0118	9.95E-12	1
rs9385403	6	127083941	26	126525715	127369230	T	C	0.2147	RPS4XP9	intergenic	-0.1216	0.0155	3.95E-15	-0.0973	0.0322	2.48E-03	-0.0799	0.0118	1.15E-11	1
rs13212467	6	127086138	26	126525715	127369230	A	G	0.2147	RPS4XP9	intergenic	-0.1213	0.0155	5.42E-15	-0.0984	0.0322	2.22E-03	-0.0802	0.0118	1.02E-11	1
rs72971190	6	127088303	26	126525715	127369230	A	G	0.2157	RPS4XP9	intergenic	0.1174	0.0154	2.85E-14	0.0974	0.0323	2.57E-03	0.0820	0.0116	1.96E-12	1
rs72971192	6	127088318	26	126525715	127369230	T	C	0.2157	RPS4XP9	intergenic	0.118	0.0154	2.14E-14	0.0985	0.0323	2.32E-03	0.0819	0.0116	1.97E-12	1
rs4897189	6	127088550	26	126525715	127369230	A	T	0.2167	RPS4XP9	intergenic	0.1183	0.0154	1.56E-14	0.0993	0.0321	1.98E-03	0.0819	0.0116	1.99E-12	1
rs9385404	6	127088591	26	126525715	127369230	A	G	0.2167	RPS4XP9	intergenic	0.1186	0.0154	1.33E-14	0.0981	0.0321	2.24E-03	0.0820	0.0116	1.78E-12	1
rs2223739	6	127089401	26	126525715	127369230	T	C	0.2157	RPS4XP9	intergenic	-0.1189	0.0154	1.17E-14	-0.0994	0.0321	1.97E-03	-0.0819	0.0116	1.98E-12	1
rs76611955	6	127090025	26	126525715	127369230	A	T	0.02684	RPS4XP9	intergenic	0.2416	0.0392	6.92E-10	0.1307	0.0698	6.10E-02	0.2160	0.0369	4.92E-09	0
rs4895815	6	127090469	26	126525715	127369230	A	G	0.2157	RPS4XP9	intergenic	0.1186	0.0154	1.33E-14	0.0977	0.0322	2.43E-03	0.0817	0.0116	2.22E-12	1
rs17054064	6	127091354	26	126525715	127369230	T	C	0.2157	RPS4XP9	intergenic	-0.119	0.0154	1.09E-14	-0.0995	0.0321	1.95E-03	-0.0815	0.0116	2.35E-12	1
rs4895816	6	127094587	26	126525715	127369230	A	C	0.2157	RPS4XP9	intergenic	0.1191	0.0154	9.88E-15	0.1001	0.0321	1.85E-03	0.0818	0.0116	1.95E-12	1
rs4895817	6	127094898	26	126525715	127369230	T	C	0.2157	RPS4XP9	intergenic	0.1191	0.0154	1.02E-14	0.1001	0.0321	1.83E-03	0.0821	0.0116	1.61E-12	1
rs9388517	6	127095666	26	126525715	127369230	A	G	0.2157	RPS4XP9	intergenic	0.1192	0.0154	9.85E-15	0.0996	0.0322	1.99E-03	0.0822	0.0116	1.56E-12	1
rs9401907	6	127096181	26	126525715	127369230	T	C	0.2167	RPS4XP9	intergenic	0.1189	0.0154	1.14E-14	0.1007	0.0322	1.78E-03	0.0821	0.0116	1.68E-12	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs983741	6	127096527	26	126525715	127369230	A	C	0.2157	RPS4XP9	intergenic	-0.1198	0.0154	7.63E-15	-0.1004	0.0323	1.85E-03	-0.0826	0.0116	1.28E-12	1
rs9375460	6	127149538	26	126525715	127369230	T	C	0.2237	RPS4XP9	intergenic	-0.1254	0.016	4.14E-15	-0.1109	0.0324	6.14E-04	-0.0865	0.0124	3.05E-12	1
rs77598707	6	127176330	26	126525715	127369230	T	C	0.02485	RPS4XP9	intergenic	-0.2513	0.0396	2.10E-10	-0.1423	0.0716	4.68E-02	-0.2015	0.0359	1.98E-08	1
rs77636716	6	127179329	26	126525715	127369230	T	G	0.02485	RPS4XP9	intergenic	-0.2529	0.0396	1.70E-10	-0.1417	0.0717	4.83E-02	-0.2089	0.0363	8.63E-09	1
rs185867463	6	127182732	26	126525715	127369230	C	G	0.02485	RPS4XP9	intergenic	-0.2496	0.0404	6.48E-10	-0.1476	0.0717	3.96E-02	-0.2001	0.0384	1.85E-07	1
rs138299249	6	127183470	26	126525715	127369230	A	G	0.1968	RPS4XP9	intergenic	0.0998	0.0175	1.25E-08	0.0934	0.0348	7.26E-03	0.0795	0.0142	2.23E-08	1
rs9375476	6	127185801	26	126525715	127369230	A	G	0.2217	RPS4XP9	intergenic	-0.1253	0.0164	2.32E-14	-0.1103	0.0324	6.69E-04	-0.0865	0.0131	3.91E-11	1
rs79398770	6	127277488	26	126525715	127369230	A	G	0.02584	RSPO3	intergenic	0.2545	0.0406	3.63E-10	0.1522	0.0723	3.53E-02	NA	NA	NA	NA
rs957960	7	18877408	27	18869552	18933411	A	C	0.3638	HDAC9	intronic	0.0794	0.0136	5.15E-09	0.0989	0.0282	4.51E-04	0.0641	0.0104	6.29E-10	1
rs12536836	7	18881075	27	18869552	18933411	T	C	0.3936	HDAC9	intronic	0.0783	0.0135	6.31E-09	0.1095	0.0278	8.40E-05	0.0633	0.0103	9.38E-10	1
rs6461386	7	18883690	27	18869552	18933411	A	G	0.3658	HDAC9	intronic	0.0843	0.0139	1.23E-09	0.1019	0.0287	3.89E-04	0.0662	0.0106	4.86E-10	1
rs13245206	7	18891259	27	18869552	18933411	A	G	0.3807	HDAC9	intronic	0.0741	0.0135	3.89E-08	0.0914	0.0281	1.16E-03	0.0574	0.0103	2.38E-08	1
rs12699995	7	18897321	27	18869552	18933411	T	C	0.4175	HDAC9	intronic	0.0768	0.0134	1.03E-08	0.1114	0.0278	6.16E-05	0.0627	0.0102	7.84E-10	1
rs12699996	7	18897323	27	18869552	18933411	T	G	0.4195	HDAC9	intronic	-0.0797	0.0135	3.54E-09	-0.1113	0.0278	6.27E-05	-0.0660	0.0105	2.81E-10	1
rs6461387	7	18898305	27	18869552	18933411	A	G	0.3917	HDAC9	intronic	0.0784	0.0134	5.05E-09	0.1107	0.0279	7.39E-05	0.0630	0.0102	7.21E-10	1
rs756854	7	18903015	27	18869552	18933411	T	C	0.3976	HDAC9	intronic	0.0804	0.0135	2.29E-09	0.1080	0.0279	1.08E-04	0.0622	0.0103	1.35E-09	1
rs59987684	7	18903517	27	18869552	18933411	A	T	0.3936	HDAC9	intronic	-0.0781	0.0136	8.69E-09	-0.1091	0.0280	9.67E-05	-0.0581	0.0104	2.43E-08	1
rs55761404	7	18903580	27	18869552	18933411	A	G	0.3917	HDAC9	intronic	-0.081	0.0136	2.47E-09	-0.1070	0.0280	1.34E-04	-0.0587	0.0104	1.78E-08	1
rs34854568	7	18903818	27	18869552	18933411	A	G	0.3827	HDAC9	intronic	0.0857	0.0135	2.21E-10	0.1037	0.0279	2.02E-04	0.0661	0.0103	1.41E-10	1
rs12699998	7	18904175	27	18869552	18933411	A	G	0.3847	HDAC9	intronic	-0.0845	0.0135	4.18E-10	-0.1090	0.0279	9.23E-05	-0.0658	0.0103	1.67E-10	1
rs12699999	7	18904264	27	18869552	18933411	A	G	0.3738	HDAC9	intronic	-0.0811	0.0136	2.38E-09	-0.1115	0.0280	7.04E-05	-0.0627	0.0104	1.51E-09	1
rs12700000	7	18904337	27	18869552	18933411	T	C	0.3231	HDAC9	intronic	-0.0792	0.014	1.38E-08	-0.0837	0.0289	3.75E-03	-0.0571	0.0106	7.92E-08	1
rs12700001	7	18904400	27	18869552	18933411	C	G	0.3917	HDAC9	intronic	-0.0871	0.0136	1.33E-10	-0.1038	0.0278	1.90E-04	-0.0662	0.0103	1.32E-10	1
rs12700002	7	18905450	27	18869552	18933411	T	C	0.4175	HDAC9	intronic	-0.0816	0.0134	1.13E-09	-0.1085	0.0276	8.58E-05	-0.0660	0.0102	1.10E-10	1
rs12700003	7	18905866	27	18869552	18933411	T	C	0.4085	HDAC9	intronic	0.0796	0.0134	2.67E-09	0.1186	0.0276	1.73E-05	0.0652	0.0102	1.71E-10	1
rs6461389	7	18907030	27	18869552	18933411	T	C	0.3579	HDAC9	intronic	0.0759	0.0137	2.80E-08	0.0918	0.0283	1.17E-03	0.0558	0.0104	8.67E-08	1
rs12530943	7	18907748	27	18869552	18933411	C	G	0.3519	HDAC9	intronic	-0.075	0.0137	4.21E-08	-0.0942	0.0283	8.90E-04	-0.0567	0.0104	5.51E-08	1
rs12530969	7	18907849	27	18869552	18933411	C	G	0.3539	HDAC9	intronic	-0.0755	0.0137	3.37E-08	-0.0916	0.0283	1.21E-03	-0.0557	0.0104	9.42E-08	1
rs12536081	7	18907930	27	18869552	18933411	A	C	0.3598	HDAC9	intronic	-0.075	0.0137	3.90E-08	-0.0945	0.0281	7.87E-04	-0.0566	0.0104	5.60E-08	1
rs6973029	7	18908850	27	18869552	18933411	T	C	0.3519	HDAC9	intronic	0.0753	0.0137	3.80E-08	0.0945	0.0283	8.56E-04	0.0634	0.0104	1.27E-09	1
rs6461390	7	18910232	27	18869552	18933411	A	G	0.3857	HDAC9	intronic	-0.0817	0.0135	1.35E-09	-0.1056	0.0278	1.48E-04	-0.0661	0.0103	1.21E-10	1
rs6951144	7	18911789	27	18869552	18933411	C	G	0.3807	HDAC9	intronic	-0.0765	0.0136	1.86E-08	-0.0952	0.0280	6.81E-04	-0.0593	0.0104	1.05E-08	1
rs6951745	7	18911957	27	18869552	18933411	A	G	0.3628	HDAC9	intronic	0.0775	0.0136	1.25E-08	0.0889	0.0282	1.63E-03	0.0599	0.0104	7.92E-09	1
rs6461391	7	18912777	27	18869552	18933411	T	C	0.3827	HDAC9	intronic	0.082	0.0135	1.39E-09	0.1032	0.0280	2.26E-04	0.0667	0.0103	8.62E-11	1
rs6461392	7	18912802	27	18869552	18933411	A	G	0.3628	HDAC9	intronic	0.0775	0.0136	1.33E-08	0.0883	0.0283	1.78E-03	0.0601	0.0104	7.02E-09	1
rs10237149	7	18915426	27	18869552	18933411	A	G	0.3807	HDAC9	intronic	0.0796	0.0135	4.26E-09	0.1086	0.0281	1.12E-04	0.0723	0.0104	3.27E-12	1
rs10237366	7	18915559	27	18869552	18933411	C	G	0.3827	HDAC9	intronic	0.0815	0.0136	1.95E-09	0.1010	0.0281	3.33E-04	0.0711	0.0104	6.88E-12	1
rs10237280	7	18915666	27	18869552	18933411	T	C	0.3847	HDAC9	intronic	0.0814	0.0136	1.99E-09	0.0987	0.0281	4.54E-04	0.0713	0.0104	6.29E-12	1
rs13233322	7	18915701	27	18869552	18933411	A	C	0.3767	HDAC9	intronic	0.0768	0.0136	1.81E-08	0.1061	0.0283	1.78E-04	0.0674	0.0104	1.07E-10	1
rs10486314	7	18915874	27	18869552	18933411	A	G	0.3767	HDAC9	intronic	-0.0769	0.0136	1.72E-08	-0.1071	0.0282	1.48E-04	-0.0669	0.0105	1.56E-10	1
rs10270210	7	18920210	27	18869552	18933411	T	C	0.4354	HDAC9	intronic	-0.0745	0.0136	4.72E-08	-0.1172	0.0279	2.64E-05	-0.0667	0.0104	1.58E-10	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs12338443	9	98147278	28	98147278	98279801	T	C	0.3231	RP11-435O5.7	intergenic	-0.0788	0.0142	2.67E-08	-0.0494	0.0296	9.47E-02	-0.0518	0.0109	2.06E-06	0
rs7860361	9	98147804	28	98147278	98279801	T	C	0.3231	RP11-435O5.7	intergenic	-0.0803	0.0141	1.34E-08	-0.0523	0.0296	7.70E-02	-0.0525	0.0109	1.37E-06	0
rs35422011	9	98149355	28	98147278	98279801	A	T	0.3221	RP11-435O5.7	intergenic	-0.085	0.0154	3.13E-08	-0.0578	0.0294	4.90E-02	-0.0528	0.0110	1.51E-06	1
rs34392622	9	98150349	28	98147278	98279801	T	C	0.3221	RP11-435O5.7	intergenic	-0.0802	0.0142	1.50E-08	-0.0527	0.0296	7.51E-02	-0.0523	0.0109	1.53E-06	0
rs10993531	9	98152242	28	98147278	98279801	T	C	0.326	RP11-435O5.7	intergenic	0.0785	0.0142	3.01E-08	0.0422	0.0295	1.53E-01	0.0528	0.0109	1.25E-06	0
rs10993532	9	98152282	28	98147278	98279801	T	C	0.325	RP11-435O5.7	intergenic	0.0787	0.0142	2.72E-08	0.0449	0.0295	1.28E-01	0.0526	0.0109	1.38E-06	0
rs13289815	9	98160000	28	98147278	98279801	T	C	0.3221	RP11-435O5.7	intergenic	-0.0805	0.0142	1.48E-08	-0.0519	0.0296	8.00E-02	-0.0527	0.0109	1.40E-06	0
rs2202303	9	98163443	28	98147278	98279801	T	C	0.3221	RP11-435O5.7	intergenic	0.0804	0.0142	1.53E-08	0.0527	0.0297	7.54E-02	0.0521	0.0109	1.76E-06	0
rs7854702	9	98164782	28	98147278	98279801	T	C	0.3241	RP11-435O5.7	intergenic	-0.0802	0.0142	1.75E-08	-0.0533	0.0296	7.20E-02	-0.0520	0.0109	1.95E-06	0
rs28573122	9	98190335	28	98147278	98279801	A	G	0.3718	RP11-435O5.2	intergenic	0.0785	0.0144	4.53E-08	0.0399	0.0292	1.73E-01	0.0479	0.0111	1.75E-05	0
rs28710957	9	98192383	28	98147278	98279801	A	T	0.337	RP11-435O5.2	intergenic	-0.0868	0.0154	1.82E-08	-0.0623	0.0303	3.99E-02	-0.0547	0.0124	9.80E-06	1
rs9632916	9	98213728	28	98147278	98279801	C	G	0.2227	PTCH1	UTR3	0.1023	0.016	1.83E-10	0.1035	0.0326	1.50E-03	0.0667	0.0122	4.04E-08	1
rs9632897	9	98214367	28	98147278	98279801	A	G	0.2237	PTCH1	UTR3	0.1005	0.016	3.09E-10	0.1004	0.0323	1.88E-03	0.0665	0.0121	4.36E-08	1
rs9632898	9	98214758	28	98147278	98279801	T	C	0.2237	PTCH1	UTR3	-0.1	0.0159	3.56E-10	-0.0981	0.0323	2.38E-03	-0.0666	0.0121	4.00E-08	1
rs2134721	9	98215306	28	98147278	98279801	T	C	0.2237	PTCH1	UTR3	-0.1006	0.0159	2.68E-10	-0.0969	0.0323	2.68E-03	-0.0665	0.0121	4.31E-08	1
rs17368876	9	98222665	28	98147278	98279801	T	C	0.2237	PTCH1	intronic	-0.1015	0.0159	1.85E-10	-0.0962	0.0321	2.76E-03	-0.0659	0.0121	4.65E-08	1
rs28571635	9	98225658	28	98147278	98279801	T	C	0.2068	PTCH1	intronic	-0.1001	0.0164	1.04E-09	-0.0886	0.0330	7.23E-03	-0.0672	0.0125	8.00E-08	1
rs28394554	9	98228225	28	98147278	98279801	T	C	0.2237	PTCH1	intronic	-0.099	0.0158	3.94E-10	-0.0974	0.0320	2.38E-03	-0.0654	0.0120	4.75E-08	1
rs2274693	9	98229297	28	98147278	98279801	A	G	0.2237	PTCH1	intronic	-0.0994	0.0158	2.96E-10	-0.0952	0.0320	2.93E-03	-0.0645	0.0120	6.86E-08	1
rs28702657	9	98231908	28	98147278	98279801	A	G	0.2237	PTCH1	intronic	-0.0991	0.0158	3.14E-10	-0.0948	0.0320	3.05E-03	-0.0642	0.0119	7.74E-08	1
rs28442014	9	98234563	28	98147278	98279801	T	C	0.2237	PTCH1	intronic	-0.0992	0.0158	3.28E-10	-0.0971	0.0320	2.41E-03	-0.0647	0.0119	5.88E-08	1
rs62558340	9	98234903	28	98147278	98279801	T	C	0.2237	PTCH1	intronic	-0.0989	0.0158	3.55E-10	-0.0979	0.0320	2.21E-03	-0.0645	0.0119	6.36E-08	1
rs2066836	9	98238358	28	98147278	98279801	A	G	0.1948	PTCH1	exonic	-0.0925	0.0164	1.77E-08	-0.0818	0.0332	1.39E-02	-0.0555	0.0125	8.36E-06	1
rs2274694	9	98242112	28	98147278	98279801	A	G	0.2237	PTCH1	intronic	0.0985	0.0158	4.08E-10	0.0957	0.0320	2.78E-03	0.0644	0.0119	5.87E-08	1
rs2297087	9	98242925	28	98147278	98279801	A	G	0.2237	PTCH1	intronic	0.0981	0.0158	4.95E-10	0.0945	0.0320	3.14E-03	0.0646	0.0119	5.42E-08	1
rs28488553	9	98245855	28	98147278	98279801	T	C	0.2247	PTCH1	intronic	0.0989	0.0157	3.28E-10	0.0917	0.0320	4.18E-03	0.0640	0.0119	7.22E-08	1
rs17369383	9	98245974	28	98147278	98279801	A	G	0.2247	PTCH1	intronic	0.099	0.0157	3.14E-10	0.0916	0.0320	4.22E-03	0.0644	0.0119	5.86E-08	1
rs28504341	9	98249963	28	98147278	98279801	T	C	0.2256	PTCH1	intronic	-0.0983	0.0158	5.50E-10	-0.0969	0.0321	2.57E-03	-0.0647	0.0119	5.60E-08	1
rs28411363	9	98252313	28	98147278	98279801	T	C	0.2237	PTCH1	intronic	0.099	0.0157	3.10E-10	0.0905	0.0321	4.82E-03	0.0638	0.0119	7.91E-08	1
rs28831479	9	98254526	28	98147278	98279801	A	C	0.2475	PTCH1	intronic	-0.0888	0.0152	5.07E-09	-0.0864	0.0312	5.62E-03	-0.0573	0.0115	6.97E-07	1
rs28633576	9	98257305	28	98147278	98279801	T	C	0.2008	PTCH1:RP11-4	ncRNA_exonic	-0.1026	0.0164	4.31E-10	-0.0923	0.0334	5.72E-03	-0.0647	0.0123	1.33E-07	1
rs28468571	9	98262735	28	98147278	98279801	A	G	0.2107	PTCH1	intronic	0.0938	0.0158	3.05E-09	0.1045	0.0326	1.36E-03	0.0631	0.0119	1.13E-07	1
rs3758301	9	98272464	28	98147278	98279801	T	C	0.2078	PTCH1	intronic	0.093	0.016	6.70E-09	0.1089	0.0328	8.98E-04	0.0640	0.0120	9.42E-08	1
rs28412122	9	98273791	28	98147278	98279801	A	G	0.2097	PTCH1	intronic	-0.0932	0.0159	5.05E-09	-0.1059	0.0328	1.24E-03	-0.0648	0.0120	6.27E-08	1
rs1877456	9	98275097	28	98147278	98279801	C	G	0.2097	PTCH1	intronic	0.0931	0.0159	5.14E-09	0.1051	0.0328	1.35E-03	0.0646	0.0120	6.83E-08	1
rs28485705	9	98276105	28	98147278	98279801	C	G	0.2058	PTCH1	intronic	0.0962	0.0162	2.91E-09	0.1146	0.0330	5.16E-04	0.0660	0.0121	4.81E-08	1
rs28410513	9	98276371	28	98147278	98279801	T	G	0.2097	PTCH1:RP11-4	ncRNA_exonic	-0.0922	0.016	7.61E-09	-0.1066	0.0329	1.18E-03	-0.0648	0.0120	6.55E-08	1
rs28491365	9	98276374	28	98147278	98279801	A	T	0.2097	PTCH1:RP11-4	ncRNA_exonic	-0.0922	0.016	7.62E-09	-0.1066	0.0329	1.18E-03	-0.0647	0.0120	6.85E-08	1
rs149658356	10	102245664	29	102245664	102371946	T	C	0.0169	SEC31B	downstream	0.3262	0.0598	4.85E-08	0.1960	0.1043	6.02E-02	NA	NA	NA	NA
rs118158982	10	102324683	29	102245664	102371946	A	G	0.01988	HIF1AN	intergenic	-0.3315	0.0584	1.38E-08	-0.1571	0.0999	1.16E-01	NA	NA	NA	NA
rs78638570	10	102335663	29	102245664	102371946	A	G	0.02584	HIF1AN	intergenic	-0.3154	0.0528	2.32E-09	-0.1413	0.0934	1.30E-01	NA	NA	NA	NA

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs138740906	10	102366639	29	102245664	102371946	T	C	0.02485	HIF1AN	intergenic	-0.3267	0.0542	1.70E-09	-0.1332	0.0926	1.50E-01	NA	NA	NA	NA
rs4439488	11	30804996	30	30798255	31020084	C	G	0.2952	DCDC1	intergenic	-0.0982	0.0151	7.71E-11	-0.0713	0.0291	1.45E-02	-0.0716	0.0113	2.60E-10	1
rs614943	11	30806623	30	30798255	31020084	T	C	0.3877	DCDC1	intergenic	0.0771	0.0141	4.76E-08	0.0457	0.0278	1.00E-01	0.0648	0.0109	2.64E-09	0
rs2021807	11	30806998	30	30798255	31020084	T	C	0.3022	DCDC1	intergenic	0.0932	0.0149	4.42E-10	0.0747	0.0291	1.02E-02	0.0703	0.0114	6.06E-10	1
rs7113110	11	30807171	30	30798255	31020084	T	C	0.3022	DCDC1	intergenic	-0.0932	0.0149	4.43E-10	-0.0748	0.0291	1.01E-02	-0.0704	0.0114	5.71E-10	1
rs911268	11	30809653	30	30798255	31020084	T	C	0.3022	DCDC1	intergenic	0.0927	0.0149	4.81E-10	0.0746	0.0290	1.01E-02	0.0699	0.0113	6.83E-10	1
rs927224	11	30810665	30	30798255	31020084	T	C	0.2932	DCDC1	intergenic	0.0956	0.015	1.74E-10	0.0735	0.0291	1.15E-02	0.0704	0.0112	3.82E-10	1
rs7930532	11	30811294	30	30798255	31020084	A	G	0.2952	DCDC1	intergenic	-0.0954	0.015	1.76E-10	-0.0724	0.0291	1.27E-02	-0.0710	0.0112	2.64E-10	1
rs35194615	11	30813303	30	30798255	31020084	T	C	0.2952	DCDC1	intergenic	-0.0975	0.0149	5.46E-11	-0.0736	0.0291	1.14E-02	-0.0708	0.0112	2.45E-10	1
rs7128775	11	30816001	30	30798255	31020084	A	T	0.3887	DCDC1	intergenic	0.077	0.014	3.50E-08	0.0469	0.0277	9.10E-02	0.0632	0.0106	2.64E-09	0
rs10835708	11	30816258	30	30798255	31020084	T	C	0.3926	DCDC1	intergenic	0.0766	0.014	4.42E-08	0.0451	0.0278	1.04E-01	0.0630	0.0107	3.34E-09	0
rs2022130	11	30819811	30	30798255	31020084	T	C	0.2962	DCDC1	intergenic	0.0981	0.0148	3.74E-11	0.0726	0.0290	1.24E-02	0.0700	0.0111	2.77E-10	1
rs507969	11	30830612	30	30798255	31020084	A	C	0.2962	DCDC1	intergenic	0.0974	0.0147	3.77E-11	0.0722	0.0290	1.28E-02	0.0685	0.0110	4.66E-10	1
rs2145795	11	30831065	30	30798255	31020084	A	G	0.3926	DCDC1	intergenic	-0.0761	0.0138	3.70E-08	-0.0445	0.0277	1.08E-01	-0.0606	0.0104	6.51E-09	0
rs7950105	11	30837058	30	30798255	31020084	T	C	0.3956	DCDC1	intergenic	-0.0736	0.0135	4.85E-08	-0.0473	0.0277	8.79E-02	-0.0574	0.0102	1.88E-08	0
rs535845	11	30839228	30	30798255	31020084	A	C	0.2962	DCDC1	intergenic	0.0945	0.0142	3.19E-11	0.0733	0.0289	1.14E-02	0.0649	0.0107	1.19E-09	1
rs532202	11	30839635	30	30798255	31020084	T	C	0.2962	DCDC1	intergenic	0.0943	0.0142	3.33E-11	0.0736	0.0289	1.10E-02	0.0650	0.0107	1.15E-09	1
rs113026	11	30846842	30	30798255	31020084	A	G	0.2962	DCDC1	intergenic	0.094	0.0142	4.20E-11	0.0726	0.0289	1.20E-02	0.0650	0.0107	1.22E-09	1
NA	11	30853147	30	30798255	31020084	C	G	0.2962	DCDC1	intronic	-0.1057	0.0194	4.87E-08	-0.0726	0.0288	1.17E-02	-0.0663	0.0108	9.05E-10	1
rs604672	11	30853226	30	30798255	31020084	C	G	0.2962	DCDC1	intronic	-0.0934	0.0142	4.56E-11	-0.0723	0.0288	1.21E-02	-0.0642	0.0106	1.54E-09	1
rs2021806	11	30853618	30	30798255	31020084	A	G	0.2992	DCDC1	intronic	-0.0924	0.0142	6.58E-11	-0.0730	0.0288	1.12E-02	-0.0646	0.0106	1.19E-09	1
rs686901	11	30854334	30	30798255	31020084	C	G	0.2952	DCDC1	intronic	0.093	0.0142	5.77E-11	0.0735	0.0288	1.08E-02	0.0643	0.0106	1.43E-09	1
rs1015541	11	30854905	30	30798255	31020084	T	G	0.2992	DCDC1	intronic	-0.092	0.0142	7.99E-11	-0.0730	0.0288	1.12E-02	-0.0645	0.0106	1.27E-09	1
rs546181	11	30855237	30	30798255	31020084	T	G	0.2972	DCDC1	intronic	0.0928	0.0142	5.72E-11	0.0721	0.0288	1.23E-02	0.0640	0.0106	1.61E-09	1
rs2312068	11	30855691	30	30798255	31020084	A	G	0.2992	DCDC1	intronic	0.0925	0.0142	6.31E-11	0.0730	0.0288	1.12E-02	0.0645	0.0106	1.25E-09	1
rs7127215	11	30858131	30	30798255	31020084	A	G	0.2992	DCDC1	intronic	-0.0927	0.0142	5.86E-11	-0.0730	0.0288	1.12E-02	-0.0644	0.0106	1.31E-09	1
rs1375378	11	30859389	30	30798255	31020084	T	C	0.2992	DCDC1	intronic	-0.0926	0.0141	5.86E-11	-0.0730	0.0288	1.12E-02	-0.0644	0.0106	1.30E-09	1
rs1823307	11	30859628	30	30798255	31020084	C	G	0.2992	DCDC1	intronic	0.0939	0.0142	3.72E-11	0.0748	0.0288	9.38E-03	0.0647	0.0107	1.38E-09	1
rs1823306	11	30859760	30	30798255	31020084	A	G	0.2982	DCDC1	intronic	-0.092	0.0142	8.14E-11	-0.0730	0.0288	1.12E-02	-0.0649	0.0106	9.57E-10	1
rs2122135	11	30860112	30	30798255	31020084	T	C	0.2992	DCDC1	intronic	0.0925	0.0141	6.13E-11	0.0730	0.0288	1.13E-02	0.0642	0.0106	1.41E-09	1
rs10767877	11	30860580	30	30798255	31020084	A	G	0.3002	DCDC1	intronic	-0.0939	0.0141	3.27E-11	-0.0726	0.0288	1.16E-02	-0.0647	0.0106	1.03E-09	1
rs808471	11	30861472	30	30798255	31020084	C	G	0.2972	DCDC1	intronic	-0.0945	0.0142	2.45E-11	-0.0686	0.0288	1.71E-02	-0.0645	0.0106	1.16E-09	1
rs1028643	11	30861880	30	30798255	31020084	A	G	0.3002	DCDC1	intronic	0.094	0.0142	3.02E-11	0.0714	0.0288	1.31E-02	0.0647	0.0106	1.07E-09	1
rs273558	11	30864319	30	30798255	31020084	A	G	0.3012	DCDC1	intronic	0.0938	0.0142	3.49E-11	0.0714	0.0288	1.31E-02	0.0647	0.0106	1.04E-09	1
rs273557	11	30864854	30	30798255	31020084	A	G	0.3002	DCDC1	intronic	-0.0943	0.0141	2.64E-11	-0.0696	0.0288	1.56E-02	-0.0650	0.0106	8.88E-10	1
rs273556	11	30866279	30	30798255	31020084	A	C	0.2962	DCDC1	intronic	0.0925	0.0142	6.57E-11	0.0723	0.0288	1.21E-02	0.0639	0.0106	1.65E-09	1
rs273555	11	30866864	30	30798255	31020084	T	C	0.2962	DCDC1	intronic	-0.0924	0.0142	6.68E-11	-0.0723	0.0288	1.21E-02	-0.0639	0.0106	1.66E-09	1
rs273554	11	30868366	30	30798255	31020084	A	G	0.2982	DCDC1	intronic	0.0936	0.0141	3.77E-11	0.0722	0.0288	1.20E-02	0.0647	0.0106	1.01E-09	1
rs273553	11	30871743	30	30798255	31020084	T	C	0.2972	DCDC1	intronic	-0.0912	0.0141	1.14E-10	-0.0758	0.0288	8.42E-03	-0.0639	0.0106	1.61E-09	1
rs273552	11	30872241	30	30798255	31020084	T	C	0.2962	DCDC1	intronic	0.0922	0.0142	7.29E-11	0.0723	0.0288	1.20E-02	0.0637	0.0106	1.80E-09	1
rs273551	11	30872579	30	30798255	31020084	A	C	0.2972	DCDC1	intronic	0.0914	0.0141	1.06E-10	0.0764	0.0288	7.97E-03	0.0637	0.0106	1.79E-09	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs273550	11	30873650	30	30798255	31020084	T	C	0.2972	DCDC1	intronic	0.0928	0.0142	6.26E-11	0.0764	0.0288	7.95E-03	0.0642	0.0107	2.03E-09	1
rs273597	11	30875093	30	30798255	31020084	T	C	0.2982	DCDC1	intronic	-0.0925	0.0141	6.01E-11	-0.0725	0.0288	1.17E-02	-0.0645	0.0106	1.12E-09	1
rs273594	11	30876113	30	30798255	31020084	C	G	0.3012	DCDC1	intronic	0.0901	0.0143	3.13E-10	0.0719	0.0288	1.24E-02	0.0622	0.0109	1.17E-08	1
rs273593	11	30878012	30	30798255	31020084	T	C	0.3012	DCDC1	intronic	-0.093	0.0141	4.70E-11	-0.0707	0.0288	1.40E-02	-0.0653	0.0106	7.12E-10	1
rs273592	11	30878849	30	30798255	31020084	T	C	0.3012	DCDC1	UTR3	0.093	0.0141	4.76E-11	0.0707	0.0288	1.40E-02	0.0654	0.0106	6.66E-10	1
rs273589	11	30881109	30	30798255	31020084	A	G	0.2982	DCDC1	intronic	-0.0944	0.0142	3.48E-11	-0.0738	0.0288	1.05E-02	-0.0664	0.0108	7.19E-10	1
rs273587	11	30883876	30	30798255	31020084	A	T	0.2922	DCDC1	intronic	-0.0929	0.0142	6.78E-11	-0.0706	0.0291	1.52E-02	-0.0648	0.0107	1.27E-09	1
rs273582	11	30890857	30	30798255	31020084	T	C	0.2982	DCDC1	intronic	0.0926	0.0141	5.83E-11	0.0678	0.0287	1.83E-02	0.0649	0.0106	9.07E-10	1
rs612171	11	30893425	30	30798255	31020084	A	G	0.3012	DCDC1	intronic	0.0894	0.0142	2.81E-10	0.0738	0.0287	1.03E-02	0.0643	0.0107	1.69E-09	1
rs273618	11	30894383	30	30798255	31020084	A	G	0.3052	DCDC1	intronic	-0.0909	0.0141	1.17E-10	-0.0720	0.0287	1.22E-02	-0.0651	0.0106	8.01E-10	1
rs273617	11	30895612	30	30798255	31020084	T	C	0.3012	DCDC1	intronic	-0.0904	0.0141	1.56E-10	-0.0739	0.0287	1.01E-02	-0.0644	0.0106	1.24E-09	1
rs273616	11	30896283	30	30798255	31020084	T	C	0.2992	DCDC1	intronic	0.0903	0.0141	1.61E-10	0.0737	0.0287	1.03E-02	0.0643	0.0106	1.35E-09	1
rs273615	11	30899836	30	30798255	31020084	A	C	0.2992	DCDC1	intronic	-0.0911	0.0141	1.12E-10	-0.0737	0.0287	1.03E-02	-0.0641	0.0106	1.67E-09	1
rs273614	11	30901982	30	30798255	31020084	A	G	0.3022	DCDC1	intronic	-0.088	0.0145	1.21E-09	-0.0706	0.0287	1.39E-02	-0.0649	0.0106	9.63E-10	1
rs273613	11	30902893	30	30798255	31020084	T	C	0.3032	DCDC1	intronic	-0.0924	0.0141	5.67E-11	-0.0705	0.0287	1.40E-02	-0.0651	0.0106	8.51E-10	1
rs273612	11	30903063	30	30798255	31020084	A	G	0.2962	DCDC1	intronic	0.092	0.0142	8.65E-11	0.0732	0.0287	1.08E-02	0.0653	0.0107	9.18E-10	1
rs273579	11	30908049	30	30798255	31020084	T	C	0.2992	DCDC1	intronic	-0.092	0.0141	7.97E-11	-0.0721	0.0287	1.20E-02	-0.0652	0.0107	9.84E-10	1
rs273576	11	30910036	30	30798255	31020084	A	G	0.2992	DCDC1	intronic	-0.0922	0.0142	7.35E-11	-0.0720	0.0287	1.21E-02	-0.0638	0.0107	2.65E-09	1
rs273573	11	30910991	30	30798255	31020084	A	C	0.2992	DCDC1	intronic	-0.0921	0.0141	6.70E-11	-0.0720	0.0287	1.21E-02	-0.0643	0.0107	1.62E-09	1
rs273572	11	30911742	30	30798255	31020084	T	C	0.2992	DCDC1	intronic	0.0922	0.0141	6.52E-11	0.0720	0.0287	1.22E-02	0.0643	0.0107	1.62E-09	1
rs273571	11	30911936	30	30798255	31020084	C	G	0.2992	DCDC1	intronic	-0.0922	0.0141	6.43E-11	-0.0720	0.0287	1.22E-02	-0.0644	0.0107	1.59E-09	1
rs273569	11	30914035	30	30798255	31020084	A	G	0.2992	DCDC1	intronic	0.0923	0.0141	6.39E-11	0.0719	0.0287	1.23E-02	0.0645	0.0107	1.48E-09	1
rs273567	11	30917214	30	30798255	31020084	T	C	0.3052	DCDC1	intronic	0.0938	0.0141	2.88E-11	0.0683	0.0287	1.74E-02	0.0646	0.0107	1.38E-09	1
rs273565	11	30918425	30	30798255	31020084	A	G	0.3022	DCDC1	intronic	0.093	0.0141	4.44E-11	0.0702	0.0288	1.48E-02	0.0640	0.0107	1.92E-09	1
rs273564	11	30918860	30	30798255	31020084	A	G	0.3022	DCDC1	intronic	-0.0935	0.0142	4.12E-11	-0.0701	0.0288	1.48E-02	-0.0640	0.0107	2.37E-09	1
rs273563	11	30919884	30	30798255	31020084	A	G	0.3042	DCDC1	intronic	0.0938	0.0141	3.10E-11	0.0685	0.0288	1.73E-02	0.0643	0.0107	1.64E-09	1
rs273562	11	30920430	30	30798255	31020084	A	T	0.3042	DCDC1	intronic	-0.0937	0.0141	3.20E-11	-0.0663	0.0288	2.11E-02	-0.0646	0.0107	1.32E-09	1
rs273560	11	30922081	30	30798255	31020084	T	C	0.3042	DCDC1	intronic	0.0937	0.0141	3.23E-11	0.0663	0.0288	2.11E-02	0.0646	0.0107	1.41E-09	1
rs273559	11	30923223	30	30798255	31020084	T	C	0.3012	DCDC1	intronic	0.0929	0.0141	4.67E-11	0.0700	0.0288	1.50E-02	0.0640	0.0107	2.00E-09	1
rs395032	11	30927200	30	30798255	31020084	T	C	0.3012	DCDC1	intronic	-0.0928	0.0141	4.97E-11	-0.0700	0.0288	1.50E-02	-0.0637	0.0107	2.31E-09	1
rs175399	11	30930374	30	30798255	31020084	A	C	0.3042	DCDC1	intronic	-0.0934	0.0141	3.76E-11	-0.0664	0.0288	2.11E-02	-0.0643	0.0107	1.68E-09	1
rs175398	11	30930393	30	30798255	31020084	T	G	0.3042	DCDC1	intronic	-0.0934	0.0141	3.80E-11	-0.0664	0.0288	2.11E-02	-0.0642	0.0107	1.76E-09	1
rs273603	11	30931904	30	30798255	31020084	T	C	0.3052	DCDC1	intronic	0.0931	0.0141	4.24E-11	0.0667	0.0288	2.03E-02	0.0643	0.0107	1.72E-09	1
rs273601	11	30933646	30	30798255	31020084	T	C	0.3062	DCDC1	intronic	0.0917	0.0141	8.38E-11	0.0683	0.0288	1.76E-02	0.0641	0.0107	1.95E-09	1
rs172073	11	30934274	30	30798255	31020084	T	C	0.3052	DCDC1	intronic	-0.0921	0.0141	7.07E-11	-0.0677	0.0288	1.87E-02	-0.0641	0.0107	1.87E-09	1
rs273610	11	30938218	30	30798255	31020084	A	G	0.3062	DCDC1	intronic	0.0924	0.0141	6.12E-11	0.0675	0.0288	1.90E-02	0.0642	0.0107	1.82E-09	1
rs273608	11	30941272	30	30798255	31020084	A	C	0.3052	DCDC1	intronic	0.0924	0.0141	6.30E-11	0.0679	0.0288	1.84E-02	0.0642	0.0107	1.80E-09	1
rs163886	11	30943561	30	30798255	31020084	A	T	0.3052	DCDC1	intronic	0.093	0.0142	5.05E-11	0.0677	0.0288	1.87E-02	0.0638	0.0107	2.31E-09	1
rs163885	11	30945365	30	30798255	31020084	T	C	0.3052	DCDC1	intronic	0.0923	0.0141	6.80E-11	0.0673	0.0288	1.94E-02	0.0643	0.0107	1.81E-09	1
rs163883	11	30947248	30	30798255	31020084	A	G	0.3012	DCDC1	intronic	-0.091	0.0142	1.36E-10	-0.0701	0.0288	1.51E-02	-0.0644	0.0107	1.74E-09	1
rs163882	11	30947681	30	30798255	31020084	C	G	0.3012	DCDC1	intronic	-0.091	0.0142	1.37E-10	-0.0701	0.0288	1.50E-02	-0.0644	0.0107	1.76E-09	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs163881	11	30948244	30	30798255	31020084	T	G	0.3052	DCDC1	intronic	-0.0914	0.0141	1.04E-10	-0.0686	0.0288	1.74E-02	-0.0642	0.0107	1.89E-09	1
rs163879	11	30951674	30	30798255	31020084	T	C	0.3062	DCDC1	intronic	0.091	0.0141	1.27E-10	0.0677	0.0288	1.89E-02	0.0641	0.0107	2.00E-09	1
rs163877	11	30953608	30	30798255	31020084	A	G	0.2982	DCDC1	intronic	-0.09	0.0142	2.52E-10	-0.0706	0.0289	1.48E-02	-0.0634	0.0107	3.38E-09	1
rs156399	11	30955947	30	30798255	31020084	A	G	0.2962	DCDC1	intronic	-0.0904	0.0142	2.07E-10	-0.0717	0.0289	1.33E-02	-0.0636	0.0107	3.16E-09	1
rs163876	11	30956077	30	30798255	31020084	A	T	0.2982	DCDC1	intronic	-0.0905	0.0142	2.00E-10	-0.0706	0.0289	1.47E-02	-0.0634	0.0107	3.33E-09	1
rs158629	11	30962964	30	30798255	31020084	C	G	0.3072	DCDC1	intronic	-0.0963	0.017	1.56E-08	-0.0679	0.0288	1.85E-02	-0.0642	0.0107	1.92E-09	1
rs163854	11	30964632	30	30798255	31020084	T	G	0.3012	DCDC1	intronic	0.0901	0.0142	2.12E-10	0.0699	0.0289	1.55E-02	0.0640	0.0107	2.38E-09	1
rs273605	11	30965855	30	30798255	31020084	A	T	0.3052	DCDC1	UTR3	-0.0912	0.0142	1.19E-10	-0.0691	0.0289	1.67E-02	-0.0637	0.0107	2.62E-09	1
rs273604	11	30966112	30	30798255	31020084	A	G	0.3032	DCDC1	intronic	0.0908	0.0142	1.46E-10	0.0700	0.0289	1.53E-02	0.0639	0.0107	2.39E-09	1
rs163874	11	30970207	30	30798255	31020084	T	C	0.3012	DCDC1	intronic	0.0907	0.0142	1.59E-10	0.0698	0.0289	1.57E-02	0.0632	0.0107	3.35E-09	1
rs158505	11	30981248	30	30798255	31020084	T	C	0.3002	DCDC1	intronic	-0.0905	0.0142	1.66E-10	-0.0702	0.0289	1.51E-02	-0.0632	0.0107	3.42E-09	1
rs158582	11	30995033	30	30798255	31020084	T	C	0.2922	DCDC1	intronic	-0.0882	0.0143	6.29E-10	-0.0738	0.0292	1.14E-02	-0.0630	0.0107	4.49E-09	1
rs9667150	11	31010455	30	30798255	31020084	A	G	0.4046	DCDC1	intronic	0.0741	0.0132	2.18E-08	0.0361	0.0274	1.89E-01	0.0507	0.0100	4.38E-07	0
rs290108	11	31010962	30	30798255	31020084	T	C	0.4026	DCDC1	intronic	0.0736	0.0132	2.75E-08	0.0389	0.0275	1.56E-01	0.0502	0.0100	5.71E-07	0
rs290106	11	31012288	30	30798255	31020084	T	G	0.4026	DCDC1	intronic	0.0737	0.0133	2.68E-08	0.0390	0.0275	1.56E-01	0.0512	0.0101	3.64E-07	0
rs3102163	11	103988675	31	103985306	104041862	T	C	0.4105	PDGFD	intronic	-0.0762	0.0139	4.01E-08	-0.0754	0.0277	6.54E-03	-0.0524	0.0112	2.62E-06	1
rs1545865	11	103989190	31	103985306	104041862	T	C	0.4105	PDGFD	intronic	-0.0762	0.0139	4.27E-08	-0.0751	0.0277	6.80E-03	-0.0538	0.0112	1.52E-06	1
rs361293	11	103994966	31	103985306	104041862	A	C	0.4105	PDGFD	intronic	-0.082	0.0133	7.45E-10	-0.0758	0.0277	6.26E-03	-0.0488	0.0103	2.10E-06	1
rs361301	11	103998180	31	103985306	104041862	T	C	0.4105	PDGFD	intronic	-0.0812	0.0133	1.07E-09	-0.0751	0.0277	6.76E-03	-0.0485	0.0103	2.29E-06	1
rs361300	11	103998386	31	103985306	104041862	A	C	0.4115	PDGFD	intronic	0.0814	0.0133	9.55E-10	0.0749	0.0277	6.87E-03	0.0487	0.0103	2.10E-06	1
rs667801	11	104003647	31	103985306	104041862	T	C	0.4105	PDGFD	intronic	0.083	0.0133	3.93E-10	0.0757	0.0277	6.29E-03	0.0486	0.0102	1.95E-06	1
rs551198	11	104004552	31	103985306	104041862	A	G	0.4105	PDGFD	intronic	0.083	0.0133	3.77E-10	0.0763	0.0277	5.96E-03	0.0479	0.0102	2.65E-06	1
rs551300	11	104004596	31	103985306	104041862	A	G	0.4115	PDGFD	intronic	-0.0833	0.0133	3.40E-10	-0.0758	0.0277	6.26E-03	-0.0484	0.0102	2.07E-06	1
rs361273	11	104006346	31	103985306	104041862	A	G	0.4105	PDGFD	intronic	-0.0809	0.0132	8.22E-10	-0.0763	0.0277	5.97E-03	-0.0478	0.0102	2.48E-06	1
rs361270	11	104008724	31	103985306	104041862	A	C	0.4115	PDGFD	intronic	-0.0809	0.0132	8.18E-10	-0.0759	0.0277	6.16E-03	-0.0475	0.0101	2.77E-06	1
rs361269	11	104009590	31	103985306	104041862	T	C	0.4115	PDGFD	intronic	0.0809	0.0132	8.13E-10	0.0759	0.0277	6.17E-03	0.0475	0.0101	2.75E-06	1
rs361268	11	104010052	31	103985306	104041862	T	C	0.4105	PDGFD	intronic	0.0806	0.0132	9.39E-10	0.0764	0.0277	5.86E-03	0.0466	0.0101	4.20E-06	1
rs1681464	11	104012656	31	103985306	104041862	A	G	0.4105	PDGFD	intronic	-0.0829	0.0132	3.02E-10	-0.0751	0.0277	6.74E-03	-0.0469	0.0101	3.49E-06	1
rs2170719	11	104012767	31	103985306	104041862	A	G	0.4105	PDGFD	intronic	0.0826	0.0132	3.51E-10	0.0751	0.0277	6.75E-03	0.0464	0.0101	4.55E-06	1
rs2760105	13	80109867	32	79859456	80251200	A	G	0.3767	NDFIP2	intronic	-0.0744	0.0134	2.78E-08	-0.0628	0.0276	2.30E-02	-0.0407	0.0102	6.70E-05	1
rs9601242	13	80135678	32	79859456	80251200	A	C	0.4145	LINC01068	intergenic	-0.0721	0.0132	4.28E-08	-0.0637	0.0272	1.94E-02	-0.0444	0.0101	1.01E-05	1
rs73235963	13	80136940	32	79859456	80251200	A	C	0.4145	LINC01068	intergenic	-0.0723	0.0132	3.95E-08	-0.0636	0.0272	1.95E-02	-0.0444	0.0101	1.00E-05	1
rs2484343	13	80137722	32	79859456	80251200	A	G	0.4145	LINC01068	intergenic	0.0724	0.0132	3.76E-08	0.0637	0.0272	1.94E-02	0.0445	0.0101	9.77E-06	1
rs2476173	13	80139875	32	79859456	80251200	A	G	0.4145	LINC01068	intergenic	-0.0726	0.0132	3.65E-08	-0.0636	0.0272	1.95E-02	-0.0446	0.0101	9.24E-06	1
rs1208049	13	80144355	32	79859456	80251200	T	G	0.4145	LINC01068	ncRNA_intronic	-0.073	0.0132	3.18E-08	-0.0638	0.0272	1.91E-02	-0.0439	0.0101	1.37E-05	1
rs2783125	13	80157890	32	79859456	80251200	A	G	0.4105	LINC01068	intergenic	0.0732	0.0132	2.85E-08	0.0699	0.0273	1.03E-02	0.0452	0.0101	7.67E-06	1
rs2783126	13	80158701	32	79859456	80251200	T	C	0.4115	LINC01068	intergenic	-0.0732	0.0132	2.83E-08	-0.0699	0.0273	1.04E-02	-0.0451	0.0101	8.15E-06	1
rs9545142	13	80162555	32	79859456	80251200	T	C	0.4105	LINC01068	intergenic	0.0737	0.0132	2.39E-08	0.0700	0.0273	1.03E-02	0.0454	0.0101	7.21E-06	1
rs2783129	13	80168720	32	79859456	80251200	C	G	0.496	LINC01068	intergenic	-0.1062	0.0132	7.62E-16	-0.0970	0.0271	3.55E-04	NA	NA	NA	NA
rs9601248	13	80169004	32	79859456	80251200	T	C	0.4602	LINC01068	intergenic	-0.1029	0.013	2.62E-15	-0.1002	0.0272	2.24E-04	-0.0497	0.0098	4.09E-07	1
rs2783130	13	80170160	32	79859456	80251200	A	G	0.497	LINC01068	intergenic	-0.1192	0.013	4.73E-20	-0.1064	0.0270	8.43E-05	-0.0527	0.0099	9.17E-08	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs9545145	13	80173760	32	79859456	80251200	A	G	0.4702	LINC01068	intergenic	-0.1046	0.0131	1.24E-15	-0.1040	0.0270	1.20E-04	-0.0492	0.0099	6.71E-07	1
rs7319427	13	80174329	32	79859456	80251200	T	C	0.4702	LINC01068	intergenic	-0.1041	0.013	1.07E-15	-0.1040	0.0270	1.21E-04	-0.0475	0.0098	1.28E-06	1
rs6563121	13	80175000	32	79859456	80251200	T	C	0.496	LINC01068	intergenic	0.1211	0.013	1.45E-20	0.1076	0.0270	6.99E-05	0.0507	0.0099	3.17E-07	1
rs9545146	13	80175606	32	79859456	80251200	T	G	0.4284	LINC01068	intergenic	0.1034	0.0131	2.75E-15	0.0909	0.0270	7.80E-04	0.0417	0.0099	2.36E-05	1
rs928640	13	80177483	32	79859456	80251200	A	G	0.3867	LINC01068	intergenic	-0.0918	0.0133	4.45E-12	-0.0951	0.0278	6.39E-04	-0.0333	0.0100	8.85E-04	1
rs9530937	13	80177836	32	79859456	80251200	A	G	0.4115	LINC01068	intergenic	0.1053	0.0132	1.24E-15	0.0984	0.0275	3.52E-04	0.0363	0.0100	2.79E-04	1
rs2760111	13	80178344	32	79859456	80251200	T	C	0.327	LINC01068	intergenic	-0.1029	0.0147	2.80E-12	-0.0987	0.0287	5.87E-04	-0.0529	0.0114	3.71E-06	1
rs2146593	13	80180112	32	79859456	80251200	T	C	0.3429	LINC01068	intergenic	-0.0937	0.0135	4.03E-12	-0.0849	0.0281	2.58E-03	-0.0282	0.0102	5.67E-03	1
rs2146592	13	80180281	32	79859456	80251200	A	G	0.3857	LINC01068	intergenic	-0.0917	0.0133	4.82E-12	-0.0969	0.0278	4.98E-04	-0.0334	0.0100	8.62E-04	1
rs9545151	13	80182535	32	79859456	80251200	A	T	0.3429	LINC01068	intergenic	0.0938	0.0135	3.70E-12	0.0851	0.0281	2.50E-03	0.0287	0.0102	4.96E-03	1
rs1932197	13	80183353	32	79859456	80251200	C	G	0.499	LINC01068	intergenic	-0.1197	0.013	3.54E-20	-0.1063	0.0270	8.56E-05	NA	NA	NA	NA
rs7990151	13	80183985	32	79859456	80251200	A	G	0.3867	LINC01068	intergenic	-0.0919	0.0133	4.42E-12	-0.0971	0.0278	4.86E-04	-0.0341	0.0101	6.90E-04	1
rs2876741	13	80186712	32	79859456	80251200	A	T	0.3429	LINC01068	intergenic	-0.093	0.0135	5.62E-12	-0.0848	0.0281	2.57E-03	-0.0288	0.0102	4.91E-03	1
NA	13	80188088	32	79859456	80251200	A	T	0.498	LINC01068	intergenic	0.1035	0.0179	6.86E-09	0.0975	0.0273	3.56E-04	NA	NA	NA	NA
rs2093620	13	80188089	32	79859456	80251200	A	C	0.498	LINC01068	intergenic	0.1208	0.0132	5.22E-20	0.1073	0.0270	7.42E-05	0.0551	0.0101	5.19E-08	1
rs9601250	13	80188702	32	79859456	80251200	T	C	0.3648	LINC01068	intergenic	0.1037	0.0141	1.71E-13	0.1124	0.0279	5.83E-05	0.0489	0.0109	7.46E-06	1
rs9601251	13	80189717	32	79859456	80251200	T	C	0.3847	LINC01068	intergenic	-0.0904	0.0133	1.01E-11	-0.0967	0.0278	5.16E-04	-0.0348	0.0101	5.67E-04	1
rs9601252	13	80189742	32	79859456	80251200	T	C	0.3857	LINC01068	intergenic	-0.0914	0.0133	5.58E-12	-0.0966	0.0278	5.25E-04	-0.0341	0.0101	7.04E-04	1
rs4141825	13	80190848	32	79859456	80251200	A	G	0.498	LINC01068	intergenic	-0.1191	0.013	4.89E-20	-0.1069	0.0271	7.94E-05	-0.0523	0.0099	1.19E-07	1
rs9545154	13	80191817	32	79859456	80251200	C	G	0.4729	LINC01068	intergenic	-0.1239	0.0132	4.62E-21	-0.0954	0.0272	4.48E-04	NA	NA	NA	NA
rs9545155	13	80191873	32	79859456	80251200	T	C	0.498	LINC01068	intergenic	-0.1203	0.013	2.19E-20	-0.1067	0.0271	8.08E-05	-0.0528	0.0099	1.01E-07	1
rs9545156	13	80192236	32	79859456	80251200	A	G	0.498	LINC01068	intergenic	-0.1252	0.015	7.53E-17	-0.1026	0.0367	5.16E-03	-0.0528	0.0103	2.88E-07	1
rs9545158	13	80192906	32	79859456	80251200	A	G	0.498	LINC01068	intergenic	0.1203	0.013	2.71E-20	0.1066	0.0271	8.28E-05	0.0532	0.0099	8.34E-08	1
rs7997134	13	80193729	32	79859456	80251200	A	G	0.3857	LINC01068	intergenic	-0.091	0.0133	6.97E-12	-0.0973	0.0279	4.84E-04	-0.0340	0.0101	7.69E-04	1
rs2876742	13	80196829	32	79859456	80251200	T	C	0.3678	LINC01068	intergenic	-0.0907	0.0135	1.81E-11	-0.0701	0.0283	1.32E-02	-0.0470	0.0103	4.83E-06	1
rs767778	13	80197115	32	79859456	80251200	A	T	0.3668	LINC01068	intergenic	0.092	0.0135	9.12E-12	0.0706	0.0283	1.27E-02	0.0468	0.0103	5.18E-06	1
rs9318645	13	80199411	32	79859456	80251200	A	G	0.3678	LINC01068	intergenic	-0.0922	0.0135	7.90E-12	-0.0702	0.0283	1.31E-02	-0.0467	0.0103	5.41E-06	1
rs4885647	13	80199998	32	79859456	80251200	A	C	0.3668	LINC01068	intergenic	-0.0922	0.0135	7.96E-12	-0.0703	0.0283	1.29E-02	-0.0468	0.0103	5.20E-06	1
rs9545159	13	80202674	32	79859456	80251200	T	C	0.3668	LINC01068	intergenic	-0.0922	0.0135	7.85E-12	-0.0695	0.0283	1.40E-02	-0.0467	0.0103	5.45E-06	1
rs2329126	13	80203805	32	79859456	80251200	A	G	0.3668	LINC01068	intergenic	-0.092	0.0135	8.28E-12	-0.0693	0.0283	1.42E-02	-0.0466	0.0103	5.55E-06	1
rs9601256	13	80208050	32	79859456	80251200	T	C	0.3668	LINC01068	intergenic	0.0922	0.0135	7.72E-12	0.0696	0.0283	1.39E-02	0.0464	0.0103	6.19E-06	1
rs4885649	13	80208801	32	79859456	80251200	A	T	0.3668	LINC01068	intergenic	0.0921	0.0135	8.05E-12	0.0696	0.0283	1.38E-02	0.0463	0.0103	6.33E-06	1
rs9530940	13	80209455	32	79859456	80251200	A	G	0.3678	LINC01068	intergenic	0.0922	0.0135	7.35E-12	0.0696	0.0283	1.39E-02	0.0463	0.0103	6.21E-06	1
rs3920578	13	80212443	32	79859456	80251200	T	G	0.3678	LINC01068	intergenic	0.0923	0.0135	7.23E-12	0.0697	0.0282	1.36E-02	0.0463	0.0102	6.17E-06	1
rs9530941	13	80213514	32	79859456	80251200	T	C	0.3678	LINC01068	intergenic	0.0923	0.0135	7.11E-12	0.0698	0.0282	1.36E-02	0.0463	0.0102	6.17E-06	1
rs9318647	13	80216846	32	79859456	80251200	A	G	0.3688	LINC01068	intergenic	-0.092	0.0135	7.91E-12	-0.0705	0.0282	1.26E-02	-0.0466	0.0102	5.28E-06	1
rs9565516	13	80217881	32	79859456	80251200	A	T	0.341	LINC01068	intergenic	0.0802	0.0138	5.41E-09	0.0673	0.0288	1.98E-02	0.0446	0.0104	1.86E-05	1
rs12430226	13	80218239	32	79859456	80251200	A	G	0.3688	LINC01068	intergenic	0.0921	0.0135	7.57E-12	0.0705	0.0282	1.25E-02	0.0468	0.0102	4.87E-06	1
rs2181432	13	80218861	32	79859456	80251200	T	C	0.3678	LINC01068	intergenic	0.092	0.0135	8.08E-12	0.0705	0.0282	1.25E-02	0.0467	0.0103	5.19E-06	1
rs9530942	13	80219035	32	79859456	80251200	A	T	0.3678	LINC01068	intergenic	0.092	0.0135	8.16E-12	0.0705	0.0282	1.25E-02	0.0467	0.0103	5.22E-06	1
rs9574450	13	80219665	32	79859456	80251200	A	C	0.3658	LINC01068	intergenic	-0.0914	0.0135	1.12E-11	-0.0716	0.0282	1.11E-02	-0.0467	0.0103	5.22E-06	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs7994255	13	80219883	32	79859456	80251200	T	G	0.3658	LINC01068	intergenic	-0.0918	0.0135	9.12E-12	-0.0734	0.0282	9.37E-03	-0.0466	0.0103	5.47E-06	1
rs7994620	13	80220015	32	79859456	80251200	A	G	0.34	LINC01068	intergenic	-0.0797	0.0137	6.21E-09	-0.0706	0.0288	1.41E-02	-0.0443	0.0104	2.16E-05	1
rs4885652	13	80222402	32	79859456	80251200	T	C	0.34	LINC01068	intergenic	-0.0798	0.0137	6.16E-09	-0.0720	0.0288	1.23E-02	-0.0448	0.0104	1.74E-05	1
rs9574452	13	80223671	32	79859456	80251200	C	G	0.34	LINC01068	intergenic	0.0795	0.0137	7.06E-09	0.0721	0.0288	1.22E-02	0.0447	0.0104	1.83E-05	1
rs4885653	13	80224421	32	79859456	80251200	T	G	0.34	LINC01068	intergenic	-0.0796	0.0137	6.62E-09	-0.0721	0.0288	1.22E-02	-0.0446	0.0104	1.87E-05	1
rs9530943	13	80226450	32	79859456	80251200	A	G	0.3688	LINC01068	intergenic	-0.0918	0.0135	9.31E-12	-0.0733	0.0283	9.52E-03	-0.0468	0.0103	5.05E-06	1
rs9545166	13	80227341	32	79859456	80251200	A	T	0.3678	LINC01068	intergenic	0.092	0.0135	8.42E-12	0.0735	0.0283	9.35E-03	0.0467	0.0103	5.40E-06	1
rs2876746	13	80231558	32	79859456	80251200	A	G	0.334	LINC01068	intergenic	-0.0781	0.0138	1.50E-08	-0.0691	0.0289	1.67E-02	-0.0437	0.0105	2.98E-05	1
rs9601258	13	80232942	32	79859456	80251200	A	G	0.341	LINC01068	intergenic	0.0793	0.0137	7.71E-09	0.0732	0.0287	1.10E-02	0.0445	0.0104	2.05E-05	1
rs2876747	13	80233541	32	79859456	80251200	T	G	0.3419	LINC01068	intergenic	0.0798	0.0137	6.35E-09	0.0726	0.0288	1.16E-02	0.0446	0.0104	1.99E-05	1
rs9318650	13	80236762	32	79859456	80251200	A	G	0.3787	LINC01068	intergenic	0.0978	0.0134	3.43E-13	0.0818	0.0282	3.71E-03	0.0444	0.0104	1.81E-05	1
rs9530944	13	80238477	32	79859456	80251200	A	C	0.3678	LINC01068	intergenic	0.092	0.0135	9.05E-12	0.0727	0.0283	1.01E-02	0.0480	0.0103	3.43E-06	1
rs9318651	13	80238557	32	79859456	80251200	T	C	0.3678	LINC01068	intergenic	-0.0922	0.0135	8.24E-12	-0.0732	0.0282	9.53E-03	-0.0477	0.0103	3.92E-06	1
rs2208938	13	80239283	32	79859456	80251200	T	C	0.3817	LINC01068	intergenic	0.0871	0.0135	1.09E-10	0.0701	0.0282	1.28E-02	0.0452	0.0103	1.24E-05	1
rs4885655	13	80240964	32	79859456	80251200	C	G	0.341	LINC01068	intergenic	-0.0795	0.0138	7.62E-09	-0.0711	0.0288	1.35E-02	-0.0460	0.0106	1.34E-05	1
rs9805769	13	80242330	32	79859456	80251200	A	C	0.3678	LINC01068	intergenic	0.092	0.0135	9.52E-12	0.0732	0.0283	9.59E-03	0.0482	0.0104	3.51E-06	1
rs2208936	13	80242608	32	79859456	80251200	C	G	0.3688	LINC01068	intergenic	0.0919	0.0135	1.02E-11	0.0715	0.0283	1.14E-02	0.0481	0.0104	3.80E-06	1
rs9574455	13	80244736	32	79859456	80251200	A	G	0.341	LINC01068	intergenic	-0.0793	0.0138	8.67E-09	-0.0713	0.0288	1.32E-02	-0.0457	0.0106	1.54E-05	1
rs4141826	13	80247791	32	79859456	80251200	A	G	0.3419	LINC01068	intergenic	-0.0782	0.0139	1.76E-08	-0.0713	0.0288	1.32E-02	-0.0462	0.0107	1.43E-05	1
rs6563129	13	80250475	32	79859456	80251200	T	C	0.3459	LINC01068	intergenic	-0.0761	0.0139	4.47E-08	-0.0715	0.0288	1.30E-02	-0.0466	0.0107	1.41E-05	1
rs2208943	13	80251200	32	79859456	80251200	T	C	0.3728	LINC01068	intergenic	0.0894	0.0137	6.20E-11	0.0744	0.0283	8.53E-03	0.0494	0.0106	3.29E-06	1
rs61976308	14	59449138	33	59449138	59891607	A	G	0.0497	RP11-112J1.2	ncRNA_intronic	-0.1742	0.0273	1.69E-10	-0.1848	0.0550	7.83E-04	-0.0433	0.0217	4.59E-02	1
rs80223023	14	59450602	33	59449138	59891607	A	C	0.05169	RP11-112J1.2	ncRNA_intronic	0.1789	0.0266	1.71E-11	0.1726	0.0548	1.65E-03	0.0545	0.0206	8.10E-03	1
rs61976311	14	59456583	33	59449138	59891607	A	G	0.0507	RP11-112J1.2	ncRNA_intronic	-0.1811	0.0264	6.84E-12	-0.1828	0.0548	8.48E-04	-0.0545	0.0204	7.47E-03	1
rs61976312	14	59457562	33	59449138	59891607	T	C	0.05169	RP11-112J1.2	ncRNA_intronic	0.1818	0.0264	5.42E-12	0.1794	0.0547	1.05E-03	0.0550	0.0203	6.85E-03	1
rs61976313	14	59459140	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	0.1809	0.0262	5.53E-12	0.1815	0.0547	9.13E-04	0.0553	0.0203	6.39E-03	1
rs61976314	14	59464840	33	59449138	59891607	C	G	0.05268	RP11-112J1.2	ncRNA_intronic	0.1812	0.0262	4.67E-12	0.1808	0.0547	9.56E-04	0.0555	0.0202	5.99E-03	1
rs61976316	14	59465860	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1805	0.0262	5.81E-12	-0.1808	0.0547	9.59E-04	-0.0544	0.0202	7.07E-03	1
rs79329625	14	59466003	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1805	0.0262	5.74E-12	-0.1807	0.0547	9.62E-04	-0.0545	0.0202	7.00E-03	1
rs112851448	14	59466077	33	59449138	59891607	T	G	0.05169	RP11-112J1.2	ncRNA_intronic	0.1801	0.0262	6.26E-12	0.1806	0.0547	9.71E-04	0.0541	0.0202	7.43E-03	1
rs61976317	14	59466439	33	59449138	59891607	T	C	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1798	0.0262	6.77E-12	-0.1807	0.0547	9.62E-04	-0.0546	0.0202	6.83E-03	1
rs61976318	14	59466465	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1804	0.0262	5.84E-12	-0.1807	0.0547	9.62E-04	-0.0544	0.0202	7.10E-03	1
rs17833470	14	59466834	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1794	0.0262	7.02E-12	-0.1809	0.0547	9.54E-04	-0.0555	0.0201	5.83E-03	1
rs117399967	14	59467126	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1819	0.0262	4.01E-12	-0.1775	0.0547	1.19E-03	-0.0541	0.0202	7.25E-03	1
rs112688994	14	59467454	33	59449138	59891607	A	C	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1801	0.0262	5.96E-12	-0.1807	0.0547	9.51E-04	-0.0550	0.0202	6.43E-03	1
rs61976319	14	59468299	33	59449138	59891607	T	C	0.05169	RP11-112J1.2	ncRNA_intronic	0.1809	0.0263	5.81E-12	0.1774	0.0548	1.20E-03	0.0541	0.0202	7.41E-03	1
rs77891125	14	59470430	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1795	0.0261	6.64E-12	-0.1806	0.0547	9.75E-04	-0.0545	0.0201	6.69E-03	1
rs61976321	14	59470576	33	59449138	59891607	A	T	0.05169	RP11-112J1.2	ncRNA_intronic	0.1794	0.0261	6.67E-12	0.1806	0.0547	9.74E-04	0.0543	0.0201	6.98E-03	1
rs61976322	14	59471046	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	0.1796	0.0261	6.35E-12	0.1806	0.0547	9.74E-04	0.0543	0.0201	6.94E-03	1
rs117483338	14	59471529	33	59449138	59891607	A	T	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1796	0.0265	1.21E-11	-0.1805	0.0547	9.75E-04	-0.0549	0.0202	6.59E-03	1
rs17095539	14	59471853	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1792	0.0261	6.95E-12	-0.1789	0.0547	1.08E-03	-0.0545	0.0201	6.72E-03	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs61976330	14	59471891	33	59449138	59891607	A	T	0.05268	RP11-112J1.2	ncRNA_intronic	0.1802	0.0261	5.23E-12	0.1806	0.0547	9.73E-04	0.0545	0.0201	6.71E-03	1
rs61976331	14	59471909	33	59449138	59891607	A	G	0.0507	RP11-112J1.2	ncRNA_intronic	0.1802	0.0261	5.27E-12	0.1806	0.0547	9.71E-04	0.0542	0.0201	7.02E-03	1
rs79690612	14	59472282	33	59449138	59891607	T	C	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1792	0.0261	6.95E-12	-0.1806	0.0547	9.74E-04	-0.0553	0.0201	6.00E-03	1
rs61976332	14	59472299	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	ncRNA_intronic	-0.1792	0.0261	6.95E-12	-0.1806	0.0547	9.74E-04	-0.0553	0.0201	6.00E-03	1
rs61976333	14	59472831	33	59449138	59891607	A	C	0.05268	RP11-112J1.2	ncRNA_intronic	0.1786	0.0261	7.95E-12	0.1828	0.0547	8.28E-04	0.0541	0.0201	7.10E-03	1
rs113935260	14	59473028	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	0.1722	0.0258	2.57E-11	0.1805	0.0547	9.76E-04	0.0485	0.0198	1.42E-02	1
rs61976335	14	59473343	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1792	0.0261	6.88E-12	-0.1805	0.0547	9.76E-04	-0.0545	0.0201	6.67E-03	1
rs59959620	14	59473840	33	59449138	59891607	A	C	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1792	0.0261	6.84E-12	-0.1805	0.0547	9.76E-04	-0.0543	0.0201	6.81E-03	1
rs61976337	14	59474677	33	59449138	59891607	C	G	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1792	0.0261	6.75E-12	-0.1805	0.0547	9.77E-04	-0.0543	0.0201	6.84E-03	1
rs77981231	14	59475229	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	ncRNA_intronic	0.1792	0.0261	6.73E-12	0.1806	0.0547	9.75E-04	0.0543	0.0201	6.81E-03	1
rs61976340	14	59479216	33	59449138	59891607	A	G	0.05268	RP11-112J1.2	ncRNA_intronic	0.1781	0.0261	8.90E-12	0.1802	0.0547	9.99E-04	0.0542	0.0200	6.86E-03	1
rs61976341	14	59479479	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1793	0.0261	6.39E-12	-0.1805	0.0547	9.81E-04	-0.0544	0.0200	6.70E-03	1
rs60607947	14	59479917	33	59449138	59891607	A	G	0.05268	RP11-112J1.2	ncRNA_intronic	0.1794	0.0261	6.29E-12	0.1805	0.0547	9.80E-04	0.0541	0.0200	6.98E-03	1
rs58324275	14	59479983	33	59449138	59891607	T	C	0.05368	RP11-112J1.2	ncRNA_intronic	0.1794	0.0261	6.16E-12	0.1800	0.0547	1.01E-03	0.0535	0.0200	7.60E-03	1
rs58966877	14	59480028	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1795	0.0261	6.13E-12	-0.1805	0.0547	9.81E-04	-0.0542	0.0200	6.81E-03	1
rs58601019	14	59480125	33	59449138	59891607	A	G	0.05268	RP11-112J1.2	ncRNA_intronic	0.1794	0.0261	6.28E-12	0.1805	0.0547	9.81E-04	0.0542	0.0200	6.80E-03	1
rs61976345	14	59480320	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1794	0.0261	6.28E-12	-0.1805	0.0547	9.81E-04	-0.0542	0.0200	6.80E-03	1
rs28464012	14	59482537	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	ncRNA_intronic	-0.1794	0.0261	6.08E-12	-0.1811	0.0547	9.41E-04	-0.0543	0.0200	6.71E-03	1
rs10146779	14	59483819	33	59449138	59891607	C	G	0.05268	RP11-112J1.2	ncRNA_intronic	0.1794	0.0261	6.19E-12	0.1806	0.0547	9.76E-04	0.0542	0.0200	6.77E-03	1
rs17255080	14	59484207	33	59449138	59891607	T	G	0.05169	RP11-112J1.2	downstream	-0.1794	0.0261	6.23E-12	-0.1806	0.0547	9.74E-04	-0.0543	0.0200	6.73E-03	1
rs10130575	14	59485903	33	59449138	59891607	A	G	0.05169	RP11-112J1.2	intergenic	-0.1792	0.0261	6.81E-12	-0.1815	0.0548	9.27E-04	-0.0535	0.0200	7.57E-03	1
rs61976347	14	59486765	33	59449138	59891607	A	G	0.0507	RP11-112J1.2	intergenic	-0.1819	0.0263	5.01E-12	-0.1758	0.0548	1.35E-03	-0.0535	0.0203	8.39E-03	1
rs10142674	14	59489070	33	59449138	59891607	C	G	0.05169	RP11-112J1.2	intergenic	0.1826	0.0263	3.76E-12	0.1852	0.0549	7.51E-04	0.0538	0.0203	8.04E-03	1
rs10132018	14	59491212	33	59449138	59891607	T	C	0.05268	RP11-112J1.2	intergenic	-0.1845	0.0262	1.98E-12	-0.1913	0.0548	4.82E-04	-0.0584	0.0202	3.74E-03	1
rs111676402	14	59505196	33	59449138	59891607	T	C	0.0507	RP11-112J1.2	intergenic	-0.184	0.0266	4.48E-12	-0.2001	0.0564	3.88E-04	-0.0641	0.0206	1.83E-03	1
rs79741821	14	59506360	33	59449138	59891607	A	C	0.0507	RP11-112J1.2	intergenic	-0.1856	0.0266	3.30E-12	-0.1985	0.0565	4.49E-04	-0.0640	0.0206	1.87E-03	1
rs79924383	14	59506790	33	59449138	59891607	A	G	0.0507	RP11-112J1.2	intergenic	-0.1848	0.0267	4.21E-12	-0.2027	0.0567	3.54E-04	-0.0640	0.0206	1.88E-03	1
rs75951218	14	59510280	33	59449138	59891607	A	T	0.0497	RP11-112J1.2	intergenic	0.1848	0.027	7.23E-12	0.2063	0.0567	2.77E-04	0.0644	0.0207	1.83E-03	1
rs17255157	14	59515491	33	59449138	59891607	T	G	0.04871	RP11-112J1.2	intergenic	0.1845	0.0269	6.87E-12	0.2039	0.0567	3.24E-04	0.0641	0.0207	1.91E-03	1
rs79830598	14	59517474	33	59449138	59891607	A	G	0.0497	RP11-112J1.2	intergenic	0.1857	0.0269	4.94E-12	0.2039	0.0567	3.25E-04	0.0653	0.0206	1.56E-03	1
rs17833596	14	59522340	33	59449138	59891607	A	T	0.0497	RP11-112J1.2	intergenic	0.1878	0.027	3.28E-12	0.2078	0.0566	2.45E-04	0.0656	0.0206	1.47E-03	1
rs17255192	14	59523309	33	59449138	59891607	A	G	0.0497	RP11-112J1.2	intergenic	0.1861	0.0269	4.43E-12	0.2078	0.0566	2.45E-04	0.0657	0.0206	1.47E-03	1
rs17833602	14	59524433	33	59449138	59891607	T	C	0.0497	RP11-112J1.2	intergenic	-0.1861	0.0269	4.47E-12	-0.2078	0.0566	2.45E-04	-0.0656	0.0206	1.48E-03	1
rs77542809	14	59524583	33	59449138	59891607	A	G	0.0497	RP11-112J1.2	intergenic	0.186	0.0269	4.49E-12	0.2078	0.0566	2.45E-04	0.0656	0.0206	1.48E-03	1
rs79187540	14	59527301	33	59449138	59891607	C	G	0.0497	RP11-112J1.2	intergenic	0.1861	0.0269	4.47E-12	0.2078	0.0566	2.45E-04	0.0653	0.0206	1.57E-03	1
rs112313693	14	59528311	33	59449138	59891607	A	G	0.0497	RP11-112J1.2	intergenic	0.1858	0.0269	4.85E-12	0.2076	0.0567	2.50E-04	0.0652	0.0206	1.59E-03	1
rs74749999	14	59528959	33	59449138	59891607	A	G	0.0497	RP11-112J1.2	intergenic	-0.186	0.0269	4.55E-12	-0.2077	0.0566	2.46E-04	-0.0653	0.0206	1.57E-03	1
rs17833614	14	59531935	33	59449138	59891607	T	C	0.0497	RP11-112J1.2	intergenic	0.186	0.0269	4.61E-12	0.2078	0.0566	2.46E-04	0.0652	0.0206	1.60E-03	1
rs75468739	14	59535773	33	59449138	59891607	A	G	0.0497	RP11-112J1.2	intergenic	-0.1859	0.0269	4.67E-12	-0.2078	0.0566	2.45E-04	-0.0651	0.0206	1.61E-03	1
rs17255213	14	59540008	33	59449138	59891607	T	C	0.0497	RP11-112J1.2	intergenic	-0.1848	0.0269	6.40E-12	-0.2176	0.0568	1.27E-04	-0.0652	0.0207	1.59E-03	1
rs17095660	14	59541935	33	59449138	59891607	T	G	0.06163	RP11-112J1.2	intergenic	0.1424	0.0245	5.92E-09	0.1809	0.0513	4.20E-04	0.0559	0.0189	3.09E-03	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs17255220	14	59543877	33	59449138	59891607	A	G	0.0497	CTD-2315A10.	intergenic	0.1849	0.0269	6.30E-12	0.2178	0.0568	1.26E-04	0.0657	0.0207	1.48E-03	1
rs74746058	14	59544253	33	59449138	59891607	T	C	0.0497	CTD-2315A10.	intergenic	-0.1852	0.0269	5.90E-12	-0.2178	0.0568	1.26E-04	-0.0666	0.0207	1.28E-03	1
rs78091436	14	59544796	33	59449138	59891607	A	G	0.0497	CTD-2315A10.	intergenic	0.1854	0.0269	5.74E-12	0.2178	0.0568	1.28E-04	0.0665	0.0207	1.31E-03	1
rs17833632	14	59547738	33	59449138	59891607	A	G	0.0497	CTD-2315A10.	intergenic	-0.1857	0.0269	5.17E-12	-0.2180	0.0568	1.25E-04	-0.0666	0.0207	1.29E-03	1
rs17833651	14	59548902	33	59449138	59891607	T	C	0.0497	CTD-2315A10.	intergenic	-0.1864	0.0269	4.40E-12	-0.2179	0.0568	1.25E-04	-0.0662	0.0207	1.38E-03	1
rs17255241	14	59549260	33	59449138	59891607	T	C	0.0497	CTD-2315A10.	intergenic	-0.1866	0.0269	4.18E-12	-0.2179	0.0568	1.25E-04	-0.0663	0.0207	1.35E-03	1
rs75666025	14	59553059	33	59449138	59891607	A	G	0.0497	CTD-2315A10.	intergenic	0.1892	0.0269	2.17E-12	0.2193	0.0569	1.16E-04	0.0676	0.0207	1.10E-03	1
rs76185024	14	59556566	33	59449138	59891607	A	T	0.04672	CTD-2315A10.	intergenic	-0.1947	0.027	5.74E-13	-0.2191	0.0573	1.33E-04	-0.0753	0.0208	2.92E-04	1
rs74742608	14	59556665	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	-0.1942	0.027	7.04E-13	-0.2192	0.0573	1.32E-04	-0.0742	0.0208	3.56E-04	1
rs79633637	14	59556931	33	59449138	59891607	A	C	0.04672	CTD-2315A10.	intergenic	0.1943	0.027	6.83E-13	0.2192	0.0573	1.32E-04	0.0739	0.0208	3.74E-04	1
rs76045330	14	59557043	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	0.1944	0.027	6.68E-13	0.2192	0.0573	1.32E-04	0.0746	0.0208	3.34E-04	1
rs17255248	14	59557419	33	59449138	59891607	T	G	0.04672	CTD-2315A10.	intergenic	0.1945	0.027	6.39E-13	0.2191	0.0573	1.32E-04	0.0743	0.0208	3.50E-04	1
rs77381622	14	59557616	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	-0.1953	0.027	5.07E-13	-0.2219	0.0572	1.07E-04	-0.0744	0.0208	3.42E-04	1
rs76443390	14	59557958	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	0.1945	0.027	6.45E-13	0.2191	0.0573	1.32E-04	0.0749	0.0208	3.15E-04	1
rs78616162	14	59558330	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	0.1946	0.027	6.25E-13	0.2191	0.0573	1.32E-04	0.0743	0.0208	3.50E-04	1
rs75499021	14	59558415	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	0.1946	0.027	6.21E-13	0.2191	0.0573	1.32E-04	0.0751	0.0208	3.02E-04	1
rs75035809	14	59558527	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	-0.1952	0.027	5.36E-13	-0.2193	0.0572	1.28E-04	-0.0756	0.0208	2.76E-04	1
rs78090044	14	59558567	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	0.1946	0.027	6.20E-13	0.2191	0.0573	1.32E-04	0.0752	0.0208	2.96E-04	1
rs1954003	14	59558892	33	59449138	59891607	A	C	0.04672	CTD-2315A10.	intergenic	-0.1946	0.027	6.19E-13	-0.2191	0.0573	1.32E-04	-0.0747	0.0208	3.24E-04	1
rs75923883	14	59559117	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	0.1947	0.027	6.18E-13	0.2191	0.0573	1.32E-04	0.0748	0.0208	3.22E-04	1
rs117513981	14	59559779	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	0.1947	0.0271	6.19E-13	0.2200	0.0573	1.25E-04	0.0738	0.0208	3.83E-04	1
rs117804823	14	59559797	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	-0.1946	0.0271	6.24E-13	-0.2200	0.0573	1.25E-04	-0.0754	0.0208	2.85E-04	1
rs75012551	14	59560013	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	0.1946	0.0271	6.31E-13	0.2200	0.0573	1.25E-04	0.0754	0.0208	2.87E-04	1
rs78339200	14	59560893	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	0.1946	0.0271	6.31E-13	0.2200	0.0573	1.25E-04	0.0755	0.0208	2.80E-04	1
rs75514756	14	59561825	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	0.1922	0.027	1.12E-12	0.2200	0.0573	1.25E-04	0.0764	0.0207	2.23E-04	1
rs78035000	14	59562075	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	-0.1947	0.0271	6.25E-13	-0.2200	0.0573	1.25E-04	-0.0772	0.0208	2.08E-04	1
rs117381419	14	59563176	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	0.1949	0.0271	6.07E-13	0.2199	0.0573	1.26E-04	0.0765	0.0208	2.39E-04	1
rs139493105	14	59563613	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	-0.1899	0.0271	2.39E-12	-0.2199	0.0573	1.27E-04	-0.0729	0.0211	5.68E-04	1
rs17833663	14	59565263	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	-0.195	0.0271	6.31E-13	-0.2151	0.0573	1.77E-04	-0.0766	0.0208	2.33E-04	1
rs76048834	14	59566092	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	-0.1954	0.0271	5.87E-13	-0.2150	0.0574	1.84E-04	-0.0764	0.0208	2.44E-04	1
rs76751566	14	59567311	33	59449138	59891607	A	G	0.04771	CTD-2315A10.	intergenic	-0.1943	0.0271	7.72E-13	-0.2115	0.0573	2.25E-04	-0.0774	0.0208	2.01E-04	1
rs74946438	14	59570172	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	-0.1951	0.0272	7.04E-13	-0.2137	0.0575	2.04E-04	-0.0771	0.0208	2.16E-04	1
rs79999583	14	59573508	33	59449138	59891607	A	G	0.04672	CTD-2315A10.	intergenic	0.195	0.0272	7.46E-13	0.2139	0.0575	2.02E-04	0.0770	0.0208	2.19E-04	1
rs78570253	14	59577898	33	59449138	59891607	T	C	0.05666	CTD-2315A10.	intergenic	-0.2027	0.026	6.21E-15	-0.2214	0.0548	5.39E-05	-0.0782	0.0200	9.03E-05	1
rs78601235	14	59578878	33	59449138	59891607	A	C	0.07256	CTD-2315A10.	intergenic	-0.2003	0.0259	1.07E-14	-0.2166	0.0545	7.22E-05	-0.0756	0.0199	1.46E-04	1
rs145409503	14	59579984	33	59449138	59891607	T	C	0.04672	CTD-2315A10.	intergenic	-0.1955	0.0273	7.26E-13	-0.2143	0.0575	1.98E-04	-0.0767	0.0209	2.45E-04	1
rs17095711	14	59580311	33	59449138	59891607	A	G	0.05765	CTD-2315A10.	intergenic	-0.1996	0.0259	1.34E-14	-0.2165	0.0545	7.24E-05	-0.0769	0.0199	1.15E-04	1
rs17255290	14	59585670	33	59449138	59891607	A	T	0.1998	CTD-2315A10.	intergenic	0.1561	0.0175	5.12E-19	0.1350	0.0371	2.76E-04	0.0511	0.0132	1.14E-04	1
rs4898978	14	59585932	33	59449138	59891607	A	C	0.1859	CTD-2315A10.	intergenic	-0.1669	0.018	1.75E-20	-0.1533	0.0390	8.52E-05	-0.0567	0.0135	2.55E-05	1
rs10498487	14	59588323	33	59449138	59891607	T	C	0.1491	CTD-2315A10.	intergenic	0.1965	0.019	3.60E-25	0.1760	0.0406	1.48E-05	0.0913	0.0143	1.68E-10	1
rs72724695	14	59590174	33	59449138	59891607	A	G	0.1491	CTD-2315A10.	intergenic	0.1969	0.019	3.20E-25	0.1746	0.0406	1.71E-05	0.0903	0.0143	2.90E-10	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs17833704	14	59591082	33	59449138	59891607	A	G	0.1889	CTD-2315A10.	intergenic	0.1608	0.0178	1.94E-19	0.1521	0.0383	7.33E-05	0.0595	0.0133	7.78E-06	1
rs72724697	14	59591624	33	59449138	59891607	T	C	0.1471	CTD-2315A10.	intergenic	0.2002	0.0191	1.05E-25	0.1709	0.0409	2.92E-05	0.0873	0.0145	1.57E-09	1
rs72724702	14	59593916	33	59449138	59891607	A	C	0.1451	CTD-2315A10.	intergenic	-0.2026	0.0192	3.98E-26	-0.1748	0.0412	2.22E-05	-0.0874	0.0145	1.69E-09	1
rs55643369	14	59595245	33	59449138	59891607	T	C	0.1859	CTD-2315A10.	intergenic	0.1671	0.018	1.82E-20	0.1529	0.0389	8.61E-05	0.0569	0.0135	2.48E-05	1
rs17255304	14	59597337	33	59449138	59891607	A	G	0.1461	CTD-2315A10.	intergenic	-0.2008	0.0191	9.97E-26	-0.1833	0.0410	7.94E-06	-0.0916	0.0144	2.13E-10	1
rs72726305	14	59597408	33	59449138	59891607	A	G	0.1461	CTD-2315A10.	intergenic	-0.2008	0.0191	9.80E-26	-0.1832	0.0410	8.06E-06	-0.0920	0.0144	1.82E-10	1
rs17255311	14	59598931	33	59449138	59891607	T	C	0.1382	CTD-2315A10.	intergenic	-0.2044	0.0194	5.05E-26	-0.1963	0.0414	2.15E-06	-0.0903	0.0146	6.59E-10	1
rs77168169	14	59601064	33	59449138	59891607	A	C	0.1342	CTD-2315A10.	intergenic	-0.2193	0.0198	2.07E-28	-0.1939	0.0424	5.04E-06	-0.0974	0.0150	7.63E-11	1
rs4901898	14	59602914	33	59449138	59891607	C	G	0.1342	CTD-2315A10.	ncRNA_exonic	-0.2199	0.0199	1.63E-28	-0.1906	0.0424	6.95E-06	-0.0983	0.0150	5.46E-11	1
rs117461235	14	59605116	33	59449138	59891607	A	G	0.1372	CTD-2315A10.	intergenic	-0.2174	0.0198	4.54E-28	-0.2056	0.0426	1.44E-06	-0.0961	0.0148	7.56E-11	1
rs4258526	14	59609282	33	59449138	59891607	T	G	0.2763	CTD-2315A10.	intergenic	0.0881	0.0142	5.34E-10	0.0244	0.0302	4.18E-01	0.0373	0.0110	6.69E-04	0
rs78580207	14	59610076	33	59449138	59891607	A	T	0.1342	CTD-2315A10.	intergenic	0.2214	0.0196	1.52E-29	0.1928	0.0420	4.62E-06	0.1025	0.0149	5.52E-12	1
rs10498489	14	59610460	33	59449138	59891607	T	G	0.1342	CTD-2315A10.	intergenic	0.2214	0.0196	1.56E-29	0.1928	0.0420	4.65E-06	0.1022	0.0149	6.51E-12	1
rs17255332	14	59611735	33	59449138	59891607	C	G	0.1352	CTD-2315A10.	intergenic	-0.2216	0.0196	1.14E-29	-0.1940	0.0421	4.10E-06	-0.1030	0.0149	4.39E-12	1
rs78032956	14	59612317	33	59449138	59891607	T	C	0.1332	CTD-2315A10.	intergenic	-0.2221	0.0196	1.14E-29	-0.1940	0.0421	4.19E-06	-0.1029	0.0149	4.38E-12	1
rs79676525	14	59612800	33	59449138	59891607	A	T	0.1332	CTD-2315A10.	intergenic	0.2221	0.0196	1.18E-29	0.1943	0.0421	4.09E-06	0.1026	0.0149	5.09E-12	1
rs1438518	14	59615848	33	59449138	59891607	A	T	0.3161	CTD-2315A10.	intergenic	0.0743	0.0136	4.25E-08	0.0144	0.0289	6.17E-01	0.0321	0.0105	2.15E-03	0
rs11626333	14	59616097	33	59449138	59891607	T	C	0.3161	CTD-2315A10.	intergenic	-0.0742	0.0136	4.46E-08	-0.0144	0.0289	6.18E-01	-0.0325	0.0105	1.92E-03	0
rs4901902	14	59617080	33	59449138	59891607	A	C	0.1352	CTD-2315A10.	intergenic	0.2259	0.0195	5.43E-31	0.2000	0.0419	1.83E-06	0.1032	0.0148	3.18E-12	1
rs8005394	14	59619564	33	59449138	59891607	C	G	0.1352	CTD-2315A10.	intergenic	0.2259	0.0195	4.75E-31	0.2020	0.0417	1.33E-06	0.1030	0.0148	3.20E-12	1
rs17833752	14	59621080	33	59449138	59891607	A	G	0.1352	CTD-2315A10.	intergenic	0.2264	0.0195	4.26E-31	0.1984	0.0419	2.22E-06	0.1032	0.0148	3.24E-12	1
rs76119478	14	59622767	33	59449138	59891607	A	C	0.04573	CTD-2315A10.	intergenic	0.176	0.0306	9.03E-09	0.1491	0.0638	1.93E-02	0.1084	0.0240	6.59E-06	1
rs4901904	14	59624317	33	59449138	59891607	T	C	0.1342	CTD-2315A10.	intergenic	-0.2271	0.0196	3.74E-31	-0.2002	0.0419	1.79E-06	-0.1024	0.0148	5.33E-12	1
rs11158250	14	59625980	33	59449138	59891607	A	G	0.2107	CTD-2315A10.	intergenic	0.1414	0.0164	5.57E-18	0.1479	0.0347	2.12E-05	0.0738	0.0125	3.39E-09	1
rs73313052	14	59625997	33	59449138	59891607	A	G	0.1302	CTD-2315A10.	intergenic	-0.2388	0.0195	2.36E-34	-0.2184	0.0421	2.19E-07	-0.1139	0.0148	1.63E-14	1
rs2164950	14	59627631	33	59449138	59891607	A	G	0.1312	CTD-2315A10.	intergenic	-0.2361	0.0195	9.21E-34	-0.2096	0.0419	5.77E-07	-0.1119	0.0148	4.70E-14	1
rs74826997	14	59628609	33	59449138	59891607	T	C	0.1312	CTD-2315A10.	intergenic	0.238	0.0195	3.31E-34	0.2138	0.0419	3.55E-07	0.1126	0.0148	3.34E-14	1
rs76341705	14	59628679	33	59449138	59891607	A	G	0.1312	CTD-2315A10.	intergenic	-0.2374	0.0195	4.59E-34	-0.2146	0.0419	3.18E-07	-0.1123	0.0149	4.11E-14	1
rs2053300	14	59629611	33	59449138	59891607	T	G	0.4583	CTD-2315A10.	intergenic	0.0737	0.0132	2.52E-08	0.0972	0.0275	4.19E-04	0.0354	0.0102	4.97E-04	1
rs4898980	14	59633677	33	59449138	59891607	A	G	0.02684	CTD-2315A10.	intergenic	-0.27	0.0493	4.46E-08	-0.0836	0.0994	4.00E-01	-0.1502	0.0391	1.23E-04	0
rs1252914	14	59636409	33	59449138	59891607	T	C	0.3171	CTD-2315A10.	intergenic	0.1354	0.0142	1.62E-21	0.1124	0.0300	1.81E-04	0.0540	0.0108	6.13E-07	1
rs79814107	14	59637503	33	59449138	59891607	A	G	0.1312	CTD-2315A10.	intergenic	0.2242	0.0197	5.57E-30	0.2026	0.0424	1.83E-06	0.1020	0.0149	7.43E-12	1
rs113269922	14	59638174	33	59449138	59891607	A	G	0.1312	CTD-2315A10.	intergenic	0.2242	0.0197	5.69E-30	0.2025	0.0424	1.86E-06	0.1019	0.0149	7.64E-12	1
rs56115079	14	59642065	33	59449138	59891607	T	G	0.1312	CTD-2315A10.	intergenic	0.2222	0.0197	1.72E-29	0.1993	0.0424	2.66E-06	0.1014	0.0149	9.42E-12	1
rs112195026	14	59643002	33	59449138	59891607	A	G	0.1312	CTD-2315A10.	intergenic	0.2226	0.0197	1.34E-29	0.2022	0.0425	1.94E-06	0.1010	0.0149	1.08E-11	1
rs76850797	14	59643746	33	59449138	59891607	T	C	0.1312	CTD-2315A10.	intergenic	0.2216	0.0197	2.26E-29	0.1993	0.0424	2.64E-06	0.1012	0.0149	9.84E-12	1
rs17095819	14	59643961	33	59449138	59891607	A	G	0.165	CTD-2315A10.	intergenic	0.1804	0.0178	5.01E-24	0.1373	0.0382	3.25E-04	0.0837	0.0136	8.11E-10	1
rs78349529	14	59644286	33	59449138	59891607	A	G	0.1312	CTD-2315A10.	intergenic	0.2227	0.0197	1.27E-29	0.2024	0.0424	1.91E-06	0.1009	0.0149	1.10E-11	1
rs28673301	14	59644498	33	59449138	59891607	T	C	0.163	CTD-2315A10.	intergenic	0.1806	0.0177	1.85E-24	0.1354	0.0381	3.89E-04	0.0799	0.0135	3.01E-09	1
rs893516	14	59648738	33	59449138	59891607	T	C	0.3211	CTD-2315A10.	downstream	0.1354	0.0142	1.06E-21	0.1081	0.0300	3.12E-04	0.0527	0.0107	9.39E-07	1
rs1438521	14	59653800	33	59449138	59891607	T	C	0.167	DAAM1	intergenic	0.1794	0.0177	3.34E-24	0.1264	0.0382	9.33E-04	0.0790	0.0134	3.86E-09	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs4901906	14	59654649	33	59449138	59891607	T	C	0.1312	DAAM1	upstream	-0.2222	0.0197	1.63E-29	-0.2010	0.0425	2.31E-06	-0.1000	0.0148	1.50E-11	1
rs79360654	14	59658600	33	59449138	59891607	A	C	0.1292	DAAM1	intronic	-0.2156	0.0197	6.90E-28	-0.2014	0.0421	1.72E-06	-0.0978	0.0149	4.67E-11	1
rs11844752	14	59658725	33	59449138	59891607	A	G	0.4632	DAAM1	intronic	0.088	0.0131	1.66E-11	0.0281	0.0276	3.09E-01	0.0317	0.0099	1.45E-03	0
NA	14	59658860	33	59449138	59891607	C	G	0.04573	DAAM1	intronic	-0.2745	0.0457	1.97E-09	-0.2052	0.0723	4.54E-03	-0.1011	0.0280	3.00E-04	1
rs77618329	14	59660552	33	59449138	59891607	T	C	0.1292	DAAM1	intronic	-0.2161	0.0197	5.44E-28	-0.2014	0.0421	1.71E-06	-0.0979	0.0149	4.49E-11	1
rs76256424	14	59661266	33	59449138	59891607	C	G	0.1292	DAAM1	intronic	0.2156	0.0197	7.13E-28	0.2014	0.0421	1.72E-06	0.0978	0.0149	4.50E-11	1
rs76674533	14	59661566	33	59449138	59891607	T	C	0.1292	DAAM1	intronic	-0.2156	0.0197	7.33E-28	-0.2013	0.0421	1.73E-06	-0.0976	0.0148	4.88E-11	1
rs143720575	14	59663805	33	59449138	59891607	A	G	0.1292	DAAM1	intronic	-0.2246	0.0201	7.25E-29	-0.2013	0.0421	1.74E-06	-0.1030	0.0155	2.81E-11	1
rs1252916	14	59664984	33	59449138	59891607	T	C	0.4483	DAAM1	intronic	0.0748	0.0135	3.02E-08	0.0989	0.0279	3.89E-04	0.0226	0.0104	3.00E-02	1
rs8016570	14	59665934	33	59449138	59891607	T	C	0.4702	DAAM1	intronic	0.0888	0.0131	1.02E-11	0.0355	0.0275	1.97E-01	0.0305	0.0099	2.05E-03	0
rs78419480	14	59666074	33	59449138	59891607	C	G	0.1233	DAAM1	intronic	0.2073	0.0202	8.64E-25	0.1929	0.0427	6.52E-06	0.1000	0.0152	4.21E-11	1
rs75255901	14	59669037	33	59449138	59891607	T	C	0.1332	DAAM1	intronic	-0.2	0.0194	7.17E-25	-0.1803	0.0409	1.08E-05	-0.0930	0.0146	1.90E-10	1
rs76787422	14	59669305	33	59449138	59891607	T	C	0.1332	DAAM1	intronic	-0.2003	0.0194	6.56E-25	-0.1806	0.0410	1.06E-05	-0.0929	0.0146	1.98E-10	1
rs17255395	14	59669394	33	59449138	59891607	T	C	0.1322	DAAM1	intronic	-0.1998	0.0194	8.33E-25	-0.1806	0.0410	1.05E-05	-0.0935	0.0146	1.62E-10	1
rs55649771	14	59669948	33	59449138	59891607	A	G	0.1342	DAAM1	intronic	-0.2017	0.0196	7.19E-25	-0.1766	0.0408	1.51E-05	-0.0971	0.0148	5.57E-11	1
rs17255402	14	59672118	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	-0.1731	0.023	5.84E-14	-0.1782	0.0498	3.48E-04	-0.0881	0.0170	2.14E-07	1
rs77652087	14	59673348	33	59449138	59891607	A	C	0.08549	DAAM1	intronic	0.1726	0.023	6.50E-14	0.1809	0.0497	2.77E-04	0.0882	0.0170	2.06E-07	1
rs79530766	14	59675486	33	59449138	59891607	A	G	0.08549	DAAM1	intronic	-0.1717	0.023	9.29E-14	-0.1781	0.0498	3.52E-04	-0.0883	0.0170	2.00E-07	1
rs76957852	14	59675634	33	59449138	59891607	T	C	0.08549	DAAM1	intronic	0.1712	0.023	1.04E-13	0.1780	0.0498	3.52E-04	0.0885	0.0170	1.88E-07	1
rs76558755	14	59676851	33	59449138	59891607	T	C	0.08549	DAAM1	intronic	-0.1707	0.023	1.13E-13	-0.1785	0.0497	3.32E-04	-0.0884	0.0170	1.95E-07	1
rs77216140	14	59678685	33	59449138	59891607	T	G	0.08648	DAAM1	intronic	0.1704	0.023	1.17E-13	0.1784	0.0497	3.35E-04	0.0884	0.0170	1.90E-07	1
rs79009632	14	59681380	33	59449138	59891607	T	C	0.08549	DAAM1	intronic	0.1681	0.0229	1.92E-13	0.1811	0.0496	2.66E-04	0.0874	0.0170	2.53E-07	1
rs75841771	14	59681450	33	59449138	59891607	A	T	0.08549	DAAM1	intronic	0.1681	0.0229	1.92E-13	0.1811	0.0496	2.65E-04	0.0874	0.0170	2.52E-07	1
rs78445564	14	59683086	33	59449138	59891607	T	C	0.04771	DAAM1	intronic	0.2169	0.0336	1.13E-10	0.1581	0.0664	1.74E-02	0.0938	0.0264	3.92E-04	1
rs17833798	14	59683581	33	59449138	59891607	A	G	0.08549	DAAM1	intronic	0.1672	0.0229	2.61E-13	0.1783	0.0497	3.36E-04	0.0875	0.0170	2.45E-07	1
rs112839082	14	59683921	33	59449138	59891607	A	G	0.08549	DAAM1	intronic	-0.1671	0.0229	2.72E-13	-0.1783	0.0497	3.37E-04	-0.0870	0.0169	2.87E-07	1
rs111608226	14	59684637	33	59449138	59891607	A	G	0.08549	DAAM1	intronic	-0.1666	0.0229	3.04E-13	-0.1783	0.0497	3.36E-04	-0.0866	0.0169	3.18E-07	1
rs74874233	14	59684859	33	59449138	59891607	A	G	0.08549	DAAM1	intronic	-0.1817	0.0241	4.45E-14	-0.1824	0.0505	3.09E-04	-0.0851	0.0182	2.74E-06	1
rs77645702	14	59685139	33	59449138	59891607	T	G	0.08648	DAAM1	intronic	0.1663	0.0228	3.19E-13	0.1811	0.0496	2.65E-04	0.0868	0.0169	2.97E-07	1
rs77773396	14	59686936	33	59449138	59891607	A	C	0.08549	DAAM1	intronic	-0.1662	0.0228	3.21E-13	-0.1785	0.0497	3.32E-04	-0.0864	0.0169	3.29E-07	1
rs721069	14	59687305	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	0.1655	0.0228	3.88E-13	0.1798	0.0496	2.92E-04	0.0868	0.0169	2.93E-07	1
rs79059243	14	59688148	33	59449138	59891607	A	G	0.08549	DAAM1	intronic	0.1654	0.0228	4.03E-13	0.1811	0.0496	2.65E-04	0.0865	0.0169	3.21E-07	1
rs113971277	14	59689547	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	0.1653	0.0228	4.22E-13	0.1811	0.0496	2.64E-04	0.0863	0.0169	3.46E-07	1
rs2099637	14	59689943	33	59449138	59891607	A	C	0.08549	DAAM1	intronic	-0.1654	0.0228	4.19E-13	-0.1811	0.0496	2.66E-04	-0.0863	0.0169	3.38E-07	1
rs76786981	14	59692786	33	59449138	59891607	A	T	0.08549	DAAM1	intronic	-0.1649	0.0228	5.22E-13	-0.1811	0.0496	2.65E-04	-0.0856	0.0169	4.21E-07	1
rs17255423	14	59694225	33	59449138	59891607	C	G	0.08648	DAAM1	intronic	-0.1639	0.0228	6.89E-13	-0.1811	0.0496	2.65E-04	-0.0855	0.0169	4.28E-07	1
rs2757117	14	59694643	33	59449138	59891607	A	G	0.2376	DAAM1	intronic	-0.0961	0.0154	3.89E-10	-0.1283	0.0324	7.64E-05	-0.0428	0.0116	2.16E-04	1
rs61986025	14	59700366	33	59449138	59891607	T	C	0.09344	DAAM1	intronic	-0.1464	0.022	2.80E-11	-0.1676	0.0472	3.92E-04	-0.0751	0.0164	4.42E-06	1
rs17095915	14	59704841	33	59449138	59891607	C	G	0.09344	DAAM1	intronic	-0.1463	0.022	2.88E-11	-0.1676	0.0472	3.90E-04	-0.0747	0.0163	4.90E-06	1
rs61986027	14	59705458	33	59449138	59891607	A	G	0.09344	DAAM1	intronic	0.1465	0.022	2.58E-11	0.1702	0.0472	3.11E-04	0.0746	0.0163	4.97E-06	1
rs17095918	14	59707006	33	59449138	59891607	T	C	0.09344	DAAM1	intronic	-0.1466	0.022	2.57E-11	-0.1682	0.0472	3.72E-04	-0.0751	0.0163	4.31E-06	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs17095928	14	59708431	33	59449138	59891607	C	G	0.09443	DAAM1	intronic	-0.147	0.022	2.23E-11	-0.1707	0.0472	2.98E-04	-0.0747	0.0163	4.88E-06	1
rs144053467	14	59709313	33	59449138	59891607	A	G	0.09443	DAAM1	intronic	0.149	0.0221	1.55E-11	0.1751	0.0477	2.46E-04	0.0753	0.0164	4.24E-06	1
rs147327353	14	59709316	33	59449138	59891607	C	G	0.09443	DAAM1	intronic	0.1492	0.0221	1.45E-11	0.1751	0.0477	2.46E-04	0.0753	0.0164	4.21E-06	1
rs61986028	14	59713871	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	-0.1503	0.0226	2.98E-11	-0.1700	0.0490	5.26E-04	-0.0770	0.0168	4.62E-06	1
rs17093312	14	59715923	33	59449138	59891607	T	G	0.08648	DAAM1	intronic	-0.1493	0.0226	4.35E-11	-0.1715	0.0490	4.71E-04	-0.0763	0.0168	5.81E-06	1
rs17095939	14	59716240	33	59449138	59891607	C	G	0.08648	DAAM1	intronic	0.1492	0.0226	4.44E-11	0.1716	0.0490	4.70E-04	0.0763	0.0168	5.78E-06	1
rs17095949	14	59716875	33	59449138	59891607	A	G	0.08748	DAAM1	intronic	0.1494	0.0226	4.24E-11	0.1716	0.0490	4.69E-04	0.0763	0.0168	5.76E-06	1
rs17095951	14	59718628	33	59449138	59891607	A	G	0.08748	DAAM1	intronic	-0.1496	0.0226	3.87E-11	-0.1719	0.0490	4.59E-04	-0.0764	0.0168	5.56E-06	1
rs17095960	14	59723745	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	-0.1506	0.0226	2.83E-11	-0.1736	0.0490	3.99E-04	-0.0764	0.0168	5.46E-06	1
rs61986029	14	59724880	33	59449138	59891607	C	G	0.08748	DAAM1	intronic	0.151	0.0226	2.53E-11	0.1738	0.0490	3.92E-04	0.0760	0.0168	6.23E-06	1
rs17095972	14	59727022	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	0.1497	0.0226	3.48E-11	0.1751	0.0489	3.50E-04	0.0764	0.0168	5.45E-06	1
rs61986030	14	59728098	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	-0.1507	0.0226	2.77E-11	-0.1727	0.0490	4.32E-04	-0.0763	0.0168	5.74E-06	1
rs61986031	14	59728168	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	-0.1506	0.0226	2.83E-11	-0.1725	0.0490	4.37E-04	-0.0762	0.0168	5.87E-06	1
rs17095974	14	59728443	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	-0.1508	0.0226	2.72E-11	-0.1727	0.0490	4.31E-04	-0.0762	0.0168	5.87E-06	1
NA	14	59731359	33	59449138	59891607	T	C	0.09046	DAAM1	intronic	0.1568	0.0286	4.32E-08	0.1847	0.0476	1.07E-04	0.0784	0.0165	1.92E-06	1
rs17833876	14	59734171	33	59449138	59891607	T	C	0.09245	DAAM1	intronic	0.1497	0.022	9.84E-12	0.1729	0.0477	2.90E-04	0.0786	0.0164	1.72E-06	1
rs17255500	14	59735696	33	59449138	59891607	T	C	0.09245	DAAM1	intronic	0.1493	0.022	1.12E-11	0.1728	0.0477	2.91E-04	0.0787	0.0164	1.70E-06	1
rs17255507	14	59736657	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	0.1492	0.022	1.15E-11	0.1728	0.0477	2.91E-04	0.0787	0.0164	1.67E-06	1
rs17255514	14	59736709	33	59449138	59891607	A	T	0.09245	DAAM1	intronic	0.1492	0.022	1.13E-11	0.1730	0.0477	2.88E-04	0.0787	0.0164	1.66E-06	1
rs61986048	14	59737176	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1492	0.022	1.16E-11	-0.1730	0.0477	2.88E-04	-0.0787	0.0164	1.66E-06	1
rs17255520	14	59737475	33	59449138	59891607	A	C	0.09245	DAAM1	intronic	-0.1494	0.022	1.10E-11	-0.1728	0.0477	2.93E-04	-0.0790	0.0164	1.54E-06	1
rs17095989	14	59737859	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.148	0.022	1.60E-11	-0.1678	0.0475	4.19E-04	-0.0788	0.0164	1.60E-06	1
rs17093314	14	59738186	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1493	0.0219	1.01E-11	-0.1680	0.0475	4.15E-04	-0.0793	0.0164	1.38E-06	1
rs17095990	14	59738654	33	59449138	59891607	A	G	0.09145	DAAM1	intronic	-0.1482	0.022	1.55E-11	-0.1690	0.0476	3.85E-04	-0.0785	0.0164	1.81E-06	1
rs61986049	14	59739068	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1493	0.022	1.09E-11	-0.1729	0.0477	2.90E-04	-0.0786	0.0164	1.73E-06	1
rs17833888	14	59739970	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	0.1493	0.022	1.14E-11	0.1729	0.0477	2.89E-04	0.0785	0.0164	1.79E-06	1
rs79869391	14	59740164	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	0.1492	0.022	1.15E-11	0.1729	0.0477	2.89E-04	0.0785	0.0164	1.79E-06	1
rs17255527	14	59741542	33	59449138	59891607	A	T	0.09245	DAAM1	intronic	0.1511	0.022	6.76E-12	0.1749	0.0479	2.60E-04	0.0774	0.0164	2.50E-06	1
rs111977890	14	59744282	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1505	0.022	8.81E-12	-0.1742	0.0479	2.76E-04	-0.0776	0.0164	2.41E-06	1
rs61986052	14	59745427	33	59449138	59891607	C	G	0.09145	DAAM1	intronic	-0.1509	0.022	7.51E-12	-0.1748	0.0479	2.62E-04	-0.0780	0.0164	2.08E-06	1
rs17255534	14	59745532	33	59449138	59891607	T	C	0.09245	DAAM1	intronic	-0.1509	0.022	7.52E-12	-0.1748	0.0479	2.62E-04	-0.0776	0.0164	2.40E-06	1
rs2033795	14	59748893	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1506	0.022	8.31E-12	-0.1748	0.0479	2.61E-04	-0.0774	0.0165	2.53E-06	1
rs4296184	14	59749007	33	59449138	59891607	T	G	0.09145	DAAM1	intronic	-0.1505	0.022	8.49E-12	-0.1764	0.0478	2.27E-04	-0.0775	0.0165	2.50E-06	1
rs61986054	14	59749187	33	59449138	59891607	A	T	0.09245	DAAM1	intronic	-0.1505	0.022	8.58E-12	-0.1764	0.0478	2.27E-04	-0.0773	0.0165	2.63E-06	1
rs61986055	14	59749226	33	59449138	59891607	T	C	0.09245	DAAM1	intronic	0.1506	0.022	8.20E-12	0.1759	0.0478	2.35E-04	0.0772	0.0165	2.67E-06	1
rs61986056	14	59750695	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1504	0.022	8.89E-12	-0.1748	0.0479	2.61E-04	-0.0774	0.0165	2.57E-06	1
rs78270394	14	59752088	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	0.1507	0.022	7.98E-12	0.1748	0.0478	2.57E-04	0.0770	0.0165	2.89E-06	1
rs75555742	14	59752121	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1495	0.022	1.03E-11	-0.1749	0.0479	2.59E-04	-0.0739	0.0164	6.90E-06	1
rs61986057	14	59752957	33	59449138	59891607	T	C	0.1133	DAAM1	intronic	-0.1203	0.02	1.90E-09	-0.1286	0.0435	3.14E-03	-0.0515	0.0151	6.34E-04	1
rs61986058	14	59758165	33	59449138	59891607	A	C	0.09245	DAAM1	UTR3	0.1511	0.022	6.90E-12	0.1755	0.0478	2.42E-04	0.0766	0.0165	3.23E-06	1
rs61986059	14	59758310	33	59449138	59891607	T	G	0.09245	DAAM1	intronic	-0.1454	0.0258	1.82E-08	-0.1769	0.0478	2.14E-04	-0.0767	0.0165	3.20E-06	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs74748336	14	59758919	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1503	0.022	8.90E-12	-0.1753	0.0478	2.48E-04	-0.0766	0.0165	3.22E-06	1
rs78271461	14	59759114	33	59449138	59891607	A	C	0.09245	DAAM1	intronic	-0.1509	0.022	7.43E-12	-0.1737	0.0478	2.80E-04	-0.0766	0.0165	3.22E-06	1
rs17255548	14	59759818	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	0.1503	0.022	8.91E-12	0.1753	0.0478	2.47E-04	0.0767	0.0165	3.20E-06	1
rs10483711	14	59761126	33	59449138	59891607	T	C	0.08748	DAAM1	intronic	-0.1523	0.0227	1.81E-11	-0.1836	0.0491	1.87E-04	-0.0754	0.0168	7.48E-06	1
rs10483713	14	59762998	33	59449138	59891607	T	C	0.09145	DAAM1	intronic	0.1501	0.022	9.65E-12	0.1765	0.0477	2.20E-04	0.0765	0.0165	3.33E-06	1
rs17255583	14	59763748	33	59449138	59891607	T	C	0.09145	DAAM1	intronic	-0.1504	0.022	8.95E-12	-0.1753	0.0478	2.46E-04	-0.0766	0.0165	3.30E-06	1
rs61984460	14	59764524	33	59449138	59891607	T	C	0.09245	DAAM1	intronic	0.1503	0.022	9.17E-12	0.1768	0.0478	2.15E-04	0.0766	0.0165	3.23E-06	1
rs61984461	14	59764529	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	0.1501	0.022	9.47E-12	0.1769	0.0478	2.14E-04	0.0767	0.0165	3.23E-06	1
rs17833930	14	59764790	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1503	0.022	9.20E-12	-0.1769	0.0478	2.13E-04	-0.0767	0.0165	3.23E-06	1
rs17833942	14	59765908	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	0.1503	0.022	9.18E-12	0.1753	0.0478	2.46E-04	0.0767	0.0165	3.20E-06	1
rs76990548	14	59768101	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	-0.1528	0.0227	1.61E-11	-0.1836	0.0491	1.88E-04	-0.0756	0.0168	7.19E-06	1
rs17096046	14	59768135	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	0.1525	0.0227	1.72E-11	0.1824	0.0491	2.02E-04	0.0756	0.0168	7.07E-06	1
rs17096048	14	59768381	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	-0.1527	0.0227	1.65E-11	-0.1829	0.0490	1.93E-04	-0.0756	0.0168	7.18E-06	1
rs61984462	14	59769760	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	-0.1528	0.0227	1.57E-11	-0.1843	0.0491	1.73E-04	-0.0757	0.0168	6.94E-06	1
rs78212084	14	59770439	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	-0.1529	0.0227	1.57E-11	-0.1826	0.0491	2.03E-04	-0.0758	0.0168	6.81E-06	1
rs61984463	14	59771730	33	59449138	59891607	A	G	0.09145	DAAM1	intronic	0.1482	0.022	1.67E-11	0.1730	0.0475	2.72E-04	0.0772	0.0165	2.77E-06	1
rs75663630	14	59772068	33	59449138	59891607	A	C	0.08648	DAAM1	intronic	-0.1525	0.0227	1.72E-11	-0.1841	0.0490	1.75E-04	-0.0758	0.0168	6.65E-06	1
rs17096053	14	59772866	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	0.1506	0.0226	2.81E-11	0.1814	0.0488	2.03E-04	0.0763	0.0168	5.91E-06	1
rs17096056	14	59772986	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	-0.1508	0.0226	2.66E-11	-0.1818	0.0488	1.96E-04	-0.0763	0.0168	5.85E-06	1
rs61984464	14	59773180	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	0.1511	0.0226	2.52E-11	0.1797	0.0488	2.35E-04	0.0761	0.0168	6.17E-06	1
rs17255610	14	59775562	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1504	0.022	8.98E-12	-0.1738	0.0478	2.78E-04	-0.0770	0.0165	2.94E-06	1
rs61984489	14	59781468	33	59449138	59891607	A	G	0.09344	DAAM1	intronic	0.1491	0.022	1.24E-11	0.1717	0.0475	3.04E-04	0.0800	0.0164	1.15E-06	1
rs17096066	14	59782604	33	59449138	59891607	T	C	0.08847	DAAM1	intronic	-0.1515	0.0226	2.15E-11	-0.1789	0.0489	2.52E-04	-0.0788	0.0168	2.75E-06	1
rs10483714	14	59785346	33	59449138	59891607	A	G	0.09443	DAAM1	intronic	0.1487	0.022	1.40E-11	0.1703	0.0476	3.44E-04	0.0791	0.0164	1.49E-06	1
rs61984493	14	59785916	33	59449138	59891607	C	G	0.09344	DAAM1	intronic	-0.149	0.022	1.29E-11	-0.1705	0.0476	3.41E-04	-0.0795	0.0164	1.32E-06	1
rs78626699	14	59786434	33	59449138	59891607	A	T	0.09443	DAAM1	intronic	-0.1489	0.022	1.29E-11	-0.1698	0.0475	3.55E-04	-0.0793	0.0164	1.38E-06	1
rs45610932	14	59787325	33	59449138	59891607	C	G	0.09145	DAAM1	intronic	-0.1487	0.022	1.43E-11	-0.1718	0.0476	3.10E-04	-0.0781	0.0165	2.06E-06	1
rs17096074	14	59789892	33	59449138	59891607	T	G	0.08648	DAAM1	exonic	-0.1505	0.0226	2.82E-11	-0.1807	0.0489	2.22E-04	-0.0768	0.0168	4.91E-06	1
rs17096077	14	59790240	33	59449138	59891607	A	T	0.08648	DAAM1	intronic	-0.1504	0.0226	2.92E-11	-0.1807	0.0489	2.23E-04	-0.0767	0.0168	5.03E-06	1
rs61984494	14	59790624	33	59449138	59891607	T	C	0.08648	DAAM1	intronic	-0.1502	0.0226	3.08E-11	-0.1808	0.0489	2.22E-04	-0.0766	0.0168	5.18E-06	1
rs17096084	14	59791647	33	59449138	59891607	A	G	0.08847	DAAM1	intronic	0.1502	0.0226	3.00E-11	0.1788	0.0489	2.59E-04	0.0779	0.0168	3.48E-06	1
rs41285510	14	59797213	33	59449138	59891607	A	G	0.09245	DAAM1	intronic	-0.1476	0.022	1.99E-11	-0.1700	0.0477	3.69E-04	-0.0774	0.0165	2.57E-06	1
rs28927674	14	59797373	33	59449138	59891607	A	G	0.09245	DAAM1	exonic	-0.1473	0.022	2.14E-11	-0.1700	0.0477	3.68E-04	-0.0774	0.0165	2.55E-06	1
rs17096107	14	59800036	33	59449138	59891607	C	G	0.08946	DAAM1	intronic	-0.1491	0.0226	4.14E-11	-0.1821	0.0489	1.98E-04	-0.0769	0.0168	4.84E-06	1
rs61984497	14	59801714	33	59449138	59891607	A	G	0.1203	DAAM1	intronic	0.1215	0.0205	3.18E-09	0.1437	0.0438	1.04E-03	0.0530	0.0152	4.97E-04	1
rs17096117	14	59805355	33	59449138	59891607	C	G	0.08847	DAAM1	intronic	0.1505	0.0227	3.08E-11	0.1775	0.0490	2.93E-04	0.0793	0.0169	2.61E-06	1
rs75341124	14	59805480	33	59449138	59891607	T	C	0.04771	DAAM1	intronic	-0.2244	0.0363	6.44E-10	-0.1890	0.0695	6.53E-03	-0.1143	0.0291	8.51E-05	1
rs17096126	14	59806629	33	59449138	59891607	T	G	0.08847	DAAM1	intronic	0.1512	0.0227	2.50E-11	0.1782	0.0490	2.74E-04	0.0782	0.0170	4.19E-06	1
rs61984499	14	59815097	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	0.1418	0.0231	8.89E-10	0.2174	0.0502	1.50E-05	0.0760	0.0171	8.45E-06	1
rs17834014	14	59816026	33	59449138	59891607	A	G	0.08648	DAAM1	intronic	0.14	0.0232	1.53E-09	0.2044	0.0504	5.09E-05	0.0765	0.0171	7.47E-06	1
rs61984520	14	59816182	33	59449138	59891607	C	G	0.08648	DAAM1	intronic	0.1408	0.0232	1.28E-09	0.1976	0.0504	9.01E-05	0.0765	0.0171	7.63E-06	1

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs61984521	14	59820189	33	59449138	59891607	T	C	0.08549	DAAM1	intronic	-0.1395	0.0232	1.84E-09	-0.1992	0.0505	7.97E-05	-0.0739	0.0171	1.58E-05	1
rs61984524	14	59824249	33	59449138	59891607	C	G	0.08648	DAAM1	intronic	0.1396	0.0232	1.82E-09	0.1975	0.0505	9.24E-05	0.0757	0.0171	9.55E-06	1
rs61984526	14	59831428	33	59449138	59891607	T	C	0.08549	DAAM1	intronic	0.1414	0.0233	1.27E-09	0.1994	0.0504	7.64E-05	0.0735	0.0173	2.07E-05	1
rs45476291	14	59836655	33	59449138	59891607	A	G	0.08648	DAAM1	UTR3	0.1393	0.0233	2.10E-09	0.1997	0.0505	7.83E-05	0.0739	0.0171	1.54E-05	1
rs61984529	14	59841236	33	59449138	59891607	T	G	0.08549	DAAM1	intergenic	-0.138	0.0233	2.94E-09	-0.2051	0.0506	5.09E-05	-0.0734	0.0172	1.89E-05	1
rs61984530	14	59844320	33	59449138	59891607	A	G	0.08648	DAAM1	intergenic	0.1374	0.0233	3.54E-09	0.1973	0.0505	9.37E-05	0.0739	0.0172	1.65E-05	1
rs75061529	14	59846735	33	59449138	59891607	A	C	0.08549	DAAM1	intergenic	-0.1371	0.0233	4.09E-09	-0.1971	0.0505	9.53E-05	-0.0740	0.0172	1.66E-05	1
rs61984532	14	59846757	33	59449138	59891607	A	G	0.08648	DAAM1	intergenic	-0.1369	0.0233	4.32E-09	-0.1971	0.0505	9.53E-05	-0.0740	0.0172	1.68E-05	1
rs61984533	14	59847613	33	59449138	59891607	T	C	0.08648	DAAM1	intergenic	0.1372	0.0233	4.09E-09	0.1957	0.0505	1.09E-04	0.0742	0.0172	1.57E-05	1
rs61984534	14	59848499	33	59449138	59891607	T	C	0.08648	DAAM1	intergenic	-0.1363	0.0233	5.16E-09	-0.1988	0.0505	8.43E-05	-0.0732	0.0172	2.04E-05	1
rs61984535	14	59852007	33	59449138	59891607	T	C	0.08648	DAAM1	intergenic	-0.1408	0.0234	1.66E-09	-0.2021	0.0506	6.51E-05	-0.0734	0.0172	1.97E-05	1
rs61984536	14	59852262	33	59449138	59891607	T	C	0.08748	DAAM1	intergenic	-0.1376	0.0234	4.01E-09	-0.2025	0.0507	6.54E-05	-0.0738	0.0172	1.79E-05	1
rs61984537	14	59852500	33	59449138	59891607	T	C	0.08648	AL159140.1	intergenic	0.1382	0.0233	3.21E-09	0.2156	0.0504	1.94E-05	0.0747	0.0172	1.41E-05	1
rs78084529	14	59852629	33	59449138	59891607	C	G	0.08748	AL159140.1	intergenic	-0.1412	0.0237	2.56E-09	-0.2161	0.0503	1.79E-05	-0.0765	0.0178	1.67E-05	1
rs79863915	14	59852630	33	59449138	59891607	T	G	0.08748	AL159140.1	intergenic	-0.1412	0.0237	2.56E-09	-0.2161	0.0503	1.79E-05	-0.0765	0.0178	1.67E-05	1
rs61984538	14	59852686	33	59449138	59891607	T	C	0.08847	AL159140.1	intergenic	0.1398	0.0233	1.93E-09	0.2161	0.0503	1.79E-05	0.0746	0.0172	1.40E-05	1
rs61984539	14	59852891	33	59449138	59891607	T	C	0.08748	AL159140.1	intergenic	-0.1391	0.0233	2.36E-09	-0.2160	0.0503	1.80E-05	-0.0737	0.0172	1.78E-05	1
rs7151357	14	59853140	33	59449138	59891607	A	C	0.08748	AL159140.1	intergenic	-0.1415	0.0235	1.72E-09	-0.2161	0.0503	1.80E-05	-0.0747	0.0175	1.93E-05	1
rs73299984	14	59854408	33	59449138	59891607	T	C	0.08748	AL159140.1	intergenic	0.1393	0.0233	2.27E-09	0.2158	0.0503	1.84E-05	0.0739	0.0172	1.75E-05	1
rs61984545	14	59856978	33	59449138	59891607	A	G	0.08648	AL159140.1	intergenic	-0.1376	0.0234	4.35E-09	-0.1979	0.0506	9.24E-05	-0.0736	0.0173	1.98E-05	1
rs80264941	14	59857852	33	59449138	59891607	T	C	0.08648	AL159140.1	intergenic	0.1375	0.0234	4.19E-09	0.2002	0.0505	7.44E-05	0.0754	0.0172	1.20E-05	1
rs112171060	14	59858269	33	59449138	59891607	A	G	0.08648	AL159140.1	intergenic	0.1376	0.0234	4.13E-09	0.1992	0.0505	8.01E-05	0.0758	0.0172	1.11E-05	1
rs61985462	14	59858837	33	59449138	59891607	T	C	0.08648	AL159140.1	intergenic	0.1377	0.0234	4.06E-09	0.1988	0.0505	8.30E-05	0.0755	0.0173	1.23E-05	1
rs113855394	14	59859472	33	59449138	59891607	T	C	0.08648	AL159140.1	intergenic	0.138	0.0234	3.84E-09	0.1971	0.0505	9.65E-05	0.0761	0.0173	1.05E-05	1
rs61985463	14	59860572	33	59449138	59891607	T	C	0.08648	AL159140.1	intergenic	-0.1378	0.0234	4.00E-09	-0.1990	0.0505	8.12E-05	-0.0764	0.0173	1.00E-05	1
rs61985464	14	59860716	33	59449138	59891607	T	C	0.08648	AL159140.1	intergenic	0.1368	0.0234	5.36E-09	0.1989	0.0505	8.20E-05	0.0764	0.0173	9.81E-06	1
rs7500427	16	52545277	34	52538040	52635000	A	G	0.2793	TOX3	intronic	-0.0844	0.015	1.89E-08	-0.0705	0.0314	2.49E-02	-0.0234	0.0116	4.30E-02	1
rs9936081	16	52549646	34	52538040	52635000	A	G	0.2793	TOX3	intronic	-0.0854	0.015	1.20E-08	-0.0707	0.0314	2.43E-02	-0.0244	0.0116	3.54E-02	1
rs1345388	16	52556293	34	52538040	52635000	T	C	0.2793	TOX3	intronic	0.0863	0.015	8.14E-09	0.0719	0.0314	2.19E-02	0.0253	0.0116	2.84E-02	1
rs12918816	16	52560213	34	52538040	52635000	A	G	0.2803	TOX3	intronic	-0.0834	0.0149	2.28E-08	-0.0730	0.0314	2.01E-02	-0.0230	0.0115	4.60E-02	1
rs1362548	16	52563951	34	52538040	52635000	C	G	0.2819	TOX3	intronic	-0.0837	0.015	2.52E-08	-0.0769	0.0313	1.39E-02	-0.0210	0.0115	6.79E-02	0
rs9921569	16	52572029	34	52538040	52635000	T	C	0.2823	TOX3	intronic	0.0837	0.0148	1.66E-08	0.0792	0.0313	1.14E-02	0.0216	0.0114	5.88E-02	0
rs35850695	16	52574343	34	52538040	52635000	A	G	0.2763	TOX3	intronic	-0.0824	0.015	4.24E-08	-0.0793	0.0314	1.17E-02	-0.0212	0.0116	6.71E-02	0
rs4784223	16	52575907	34	52538040	52635000	A	G	0.2823	TOX3	intronic	0.0845	0.0148	1.23E-08	0.0796	0.0313	1.10E-02	0.0215	0.0114	5.96E-02	0
rs3095602	16	52580500	34	52538040	52635000	A	G	0.2903	TOX3	intronic	-0.0849	0.0147	8.14E-09	-0.0734	0.0313	1.90E-02	-0.0213	0.0113	5.91E-02	0
rs12930156	16	52581424	34	52538040	52635000	T	C	0.2913	TOX3	intronic	-0.0852	0.0147	7.28E-09	-0.0733	0.0312	1.90E-02	-0.0208	0.0113	6.50E-02	0
rs3095604	16	52581979	34	52538040	52635000	C	G	0.2903	TOX3	upstream	-0.085	0.0147	7.80E-09	-0.0736	0.0312	1.85E-02	-0.0210	0.0113	6.22E-02	0
rs28463809	16	52583054	34	52538040	52635000	T	G	0.2903	TOX3	intergenic	-0.0854	0.0147	6.52E-09	-0.0738	0.0312	1.81E-02	-0.0212	0.0113	5.94E-02	0
rs4784226	16	52583143	34	52538040	52635000	T	C	0.2495	TOX3	intergenic	-0.0878	0.0153	9.17E-09	-0.0691	0.0318	2.99E-02	-0.0249	0.0117	3.43E-02	1
rs3095606	16	52584173	34	52538040	52635000	A	G	0.2903	CASC16	intergenic	0.0852	0.0147	7.11E-09	0.0740	0.0312	1.78E-02	0.0211	0.0113	6.03E-02	0
rs3095607	16	52584295	34	52538040	52635000	T	G	0.2903	CASC16	intergenic	0.0852	0.0147	7.02E-09	0.0740	0.0312	1.78E-02	0.0213	0.0113	5.82E-02	0

rsID	chr	pos (hg19)	Genomic Locus	start	end	A1	A2	MAF	Nearest Genes	Function	Meta-GWAS (N = 23,784)			UKBB (N = 6,234)			ENIGMA (N = 19,152)*			Replicated**
											Beta	SE	P-value	Beta	SE	P-value	Beta	SE	P-value	
rs3112578	16	52585440	34	52538040	52635000	T	C	0.2555	CASC16	downstream	0.0886	0.015	3.84E-09	0.0713	0.0316	2.43E-02	0.0247	0.0115	3.22E-02	1
rs3803662	16	52586341	34	52538040	52635000	A	G	0.2913	CASC16	ncRNA_exonic	-0.0853	0.0147	6.07E-09	-0.0741	0.0312	1.74E-02	-0.0207	0.0112	6.52E-02	0
rs3803661	16	52586477	34	52538040	52635000	A	G	0.2913	CASC16	ncRNA_intronic	-0.0854	0.0147	5.99E-09	-0.0741	0.0312	1.74E-02	-0.0208	0.0112	6.36E-02	0
rs4784227	16	52599188	34	52538040	52635000	T	C	0.2545	CASC16	ncRNA_intronic	-0.0867	0.0153	1.41E-08	-0.0636	0.0318	4.51E-02	-0.0249	0.0118	3.49E-02	1
rs6097618	20	52448936	35	52448936	52471667	C	G	0.4433	AC006076.1	intergenic	0.0749	0.0136	3.85E-08	0.0529	0.0276	5.54E-02	0.0202	0.0104	5.28E-02	0
rs6126986	20	52464719	35	52448936	52471667	T	C	0.493	SUMO1P1	intergenic	-0.0747	0.0136	4.19E-08	-0.0307	0.0277	2.67E-01	-0.0201	0.0106	5.83E-02	0
rs720387	20	52465049	35	52448936	52471667	T	C	0.494	SUMO1P1	intergenic	0.0748	0.0136	4.18E-08	0.0332	0.0276	2.29E-01	0.0203	0.0106	5.68E-02	0
rs10432728	20	52466100	35	52448936	52471667	T	C	0.492	SUMO1P1	intergenic	-0.0785	0.0139	1.65E-08	-0.0338	0.0276	2.20E-01	-0.0238	0.0110	3.07E-02	0
rs4811476	20	52468966	35	52448936	52471667	T	C	0.496	SUMO1P1	intergenic	0.0801	0.0144	2.76E-08	0.0295	0.0274	2.82E-01	0.0235	0.0117	4.37E-02	0

* Based on genome-wide tests of inferred statistics computed from the roi-specific GWASs of cortical surface area[1] in 19,152 participants of ENIGMA study[2].

** Replicated (=1) if the effect size estimates from both 'replication' association tests have the same direction as that from the meta-GWAS and p-values < 0.05.

1 .Nieuwboer, H. A., Pool, R., Dolan, C. V., Boomsma, D. I. & Nivard, M. G. GWIS: Genome-wide inferred statistics for functions of multiple phenotypes. The American Journal of Human Genetics 99, 917–927 (2016).

2. Grasby, K. L. et al. The genetic architecture of the human cerebral cortex. bioRxiv 399402 (2018). doi:10.1101/399402

Table E5. Expression levels of *IGF2BP1*, *MAPT* and *DAAM1* measured in different brain structures from donors at different ages.
The mRNA expression levels were measured by RNA sequencing in 607 brain tissues from 18 female and 23 male donors (tabulated based on the data available at www.brainspan.org)

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB112	OFC	R	8PCW	56	M	European	5	6.94	9.8	5	USC	19.185128	58.669631	8.327997
HSB112	DFC	R	8PCW	56	M	European	5	6.94	9.8	5	USC	38.161143	51.392666	7.567156
HSB112	VFC	R	8PCW	56	M	European	5	6.94	9.8	5	USC	36.962895	60.83129	10.358724
HSB112	MFC	R	8PCW	56	M	European	5	6.94	9.8	5	USC	51.417921	45.691642	7.741614
HSB112	M1CS1C	R	8PCW	56	M	European	5	6.94	9.8	5	USC	49.744818	55.691311	10.006544
HSB112	PC	R	8PCW	56	M	European	5	6.94	9.8	5	USC	45.578767	55.845701	9.827986
HSB112	STC	R	8PCW	56	M	European	5	6.94	9.8	5	USC	31.775582	85.02453	13.497321
HSB112	ITC	R	8PCW	56	M	European	5	6.94	9.8	5	USC	25.118489	105.176149	14.35899
HSB112	OC	R	8PCW	56	M	European	5	6.94	9.8	5	USC	58.858334	39.661822	9.626848
HSB112	HIP	R	8PCW	56	M	European	5	6.94	9.8	5	USC	50.128689	30.888669	10.136228
HSB112	AMY	R	8PCW	56	M	European	5	6.94	9.8	5	USC	26.377882	104.745089	16.567088
HSB112	CGE	R	8PCW	56	M	European	5	6.94	9.8	5	USC	46.448011	42.151368	10.28541
HSB112	LGE	R	8PCW	56	M	European	5	6.94	9.8	5	USC	40.218345	69.666691	12.209589
HSB112	MGE	R	8PCW	56	M	European	5	6.94	9.8	5	USC	56.425901	52.261428	9.685202
HSB112	DTH	R	8PCW	56	M	European	5	6.94	9.8	5	USC	38.379069	104.615336	15.558806
HSB112	URL	R	8PCW	56	M	European	5	6.94	9.8	5	USC	10.883005	125.488842	18.806048
HSB148	OFC	L	9PCW	63	M	European	1	6.01	10	5	YALE	25.003865	46.362347	10.194641
HSB148	DFC	L	9PCW	63	M	European	1	6.01	10	5	YALE	26.14444	40.058138	11.475317
HSB148	MFC	L	9PCW	63	M	European	1	6.01	10	5	YALE	25.567661	42.220524	11.267463
HSB148	M1CS1C	L	9PCW	63	M	European	1	6.01	10	5	YALE	31.12397	13.744205	8.912443
HSB148	PC	L	9PCW	63	M	European	1	6.01	10	5	YALE	20.079648	62.024461	14.485067
HSB148	TC	L	9PCW	63	M	European	1	6.01	10	5	YALE	19.065342	67.480219	17.739324
HSB148	OC	L	9PCW	63	M	European	1	6.01	10	5	YALE	31.763985	44.401367	13.050194
HSB148	HIP	L	9PCW	63	M	European	1	6.01	10	5	YALE	22.512766	47.454317	12.627581
HSB148	AMY	L	9PCW	63	M	European	1	6.01	10	5	YALE	17.684082	66.994027	12.422518
HSB148	CGE	L	9PCW	63	M	European	1	6.01	10	5	YALE	26.061204	20.978255	8.160755
HSB148	LGE	L	9PCW	63	M	European	1	6.01	10	5	YALE	20.853801	42.448943	11.736687
HSB148	MGE	L	9PCW	63	M	European	1	6.01	10	5	YALE	22.064575	70.56736	10.580124
HSB148	DTH	L	9PCW	63	M	European	1	6.01	10	5	YALE	10.687644	151.577594	19.44688
HSB148	URL	L	9PCW	63	M	European	1	6.01	10	5	YALE	5.422004	140.086935	22.65548
HSB153	OFC	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	3.93903	137.531151	28.259821
HSB153	DFC	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.674605	128.752829	26.14951
HSB153	VFC	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.215799	133.66551	31.027307
HSB153	MFC	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	5.097286	140.611877	26.079327
HSB153	M1C	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.620577	130.488883	25.785253
HSB153	S1C	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.676863	132.739184	19.780301
HSB153	IPC	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.658816	124.248744	15.089575
HSB153	A1C	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.143476	130.488883	17.167598
HSB153	STC	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.929685	123.08411	15.306079
HSB153	ITC	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.527181	121.944953	16.694582
HSB153	V1C	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	5.986664	113.649795	12.509778
HSB153	HIP	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	3.457155	92.59485	8.570237
HSB153	AMY	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	7.459627	59.673873	10.441828
HSB153	STR	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	2.201668	140.611877	19.514787
HSB153	MD	R	12PCW	84	F	Asian	1	NA	9.6	5	YALE	4.854734	139.566678	17.297369
HSB150	OFC	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	7.323629	112.393186	19.810599
HSB150	DFC	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	6.625589	120.10056	18.112009
HSB150	VFC	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	6.021944	125.4398	24.501661

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB150	MFC	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	7.819183	118.425485	15.748532
HSB150	M1C	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	5.815429	130.04966	27.057511
HSB150	S1C	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	5.890185	129.181678	18.075817
HSB150	IPC	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	6.766187	131.828033	18.702728
HSB150	A1C	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	6.307669	136.539788	19.474021
HSB150	STC	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	6.351415	122.701605	18.380044
HSB150	ITC	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	7.338412	122.321897	18.589513
HSB150	V1C	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	10.462556	117.282004	16.716658
HSB150	HIP	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	11.630296	77.918026	10.376959
HSB150	AMY	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	6.538249	125.84286	17.156571
HSB150	STR	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	8.400763	112.393186	14.019839
HSB150	MD	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	4.974105	221.840074	25.303198
HSB150	CBC	R	12PCW	84	F	African	2.33	6.08	9.3	5	YALE	4.52007	183.460689	23.304143
HSB113	OFC	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	4.215614	119.374774	26.364573
HSB113	DFC	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	5.539255	112.73215	23.179041
HSB113	VFC	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	4.502982	112.475304	21.296247
HSB113	MFC	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	5.736086	126.413964	25.175533
HSB113	M1C	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	4.748686	120.276026	20.850598
HSB113	S1C	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	4.544912	124.722103	16.996746
HSB113	IPC	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	5.440538	128.523559	13.884302
HSB113	A1C	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	4.592272	120.580294	21.050523
HSB113	ITC	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	5.377568	117.62246	14.768944
HSB113	V1C	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	7.200826	109.503431	12.698091
HSB113	HIP	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	6.331349	92.59532	10.144653
HSB113	AMY	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	4.772765	124.722103	15.565239
HSB113	STR	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	5.42946	142.924426	18.791417
HSB113	MD	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	3.444929	183.437336	17.695488
HSB113	CBC	R	12PCW	84	F	African/European	4	6.92	9.5	5	USC	4.464478	129.712148	16.102524
HSB103	OFC	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	6.544475	78.599298	16.834071
HSB103	DFC	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	5.694196	106.273347	17.618864
HSB103	VFC	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	5.347549	89.846277	19.028234
HSB103	MFC	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	10.352039	63.699851	12.156976
HSB103	M1C	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	5.68262	108.790742	18.974216
HSB103	S1C	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	5.60259	106.051635	16.488502
HSB103	IPC	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	6.04046	107.399448	13.298987
HSB103	A1C	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	4.71192	105.746182	17.449427
HSB103	ITC	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	7.011365	96.074788	13.884302
HSB103	V1C	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	9.892217	91.502271	12.935681
HSB103	HIP	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	8.467135	81.588038	10.12817
HSB103	AMY	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	11.552707	81.239274	12.560658
HSB103	STR	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	5.684063	105.393335	15.1874
HSB103	CBC	R	13PCW	91	M	European	1.5	NA	9.3	5	USC	5.177215	136.68387	18.003576
HSB149	OFC	L	13PCW	91	F	European	2	6.39	10	5	YALE	4.122226	127.486323	32.522342
HSB149	DFC	L	13PCW	91	F	European	2	6.39	10	5	YALE	4.591559	123.469445	29.704147
HSB149	VFC	L	13PCW	91	F	European	2	6.39	10	5	YALE	3.625322	127.070695	31.164895
HSB149	MFC	L	13PCW	91	F	European	2	6.39	10	5	YALE	5.641661	120.464166	29.169501
HSB149	M1C	L	13PCW	91	F	European	2	6.39	10	5	YALE	3.989368	125.84286	29.689315
HSB149	S1C	L	13PCW	91	F	European	2	6.39	10	5	YALE	3.953476	129.61394	26.665326
HSB149	IPC	L	13PCW	91	F	European	2	6.39	10	5	YALE	3.862495	123.08411	20.752563
HSB149	A1C	L	13PCW	91	F	European	2	6.39	10	5	YALE	2.972139	141.141572	28.259821
HSB149	STC	L	13PCW	91	F	European	2	6.39	10	5	YALE	3.832296	115.597735	20.541546

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB149	ITC	L	13PCW	91	F	European	2	6.39	10	5	YALE	4.173935	109.38878	17.956624
HSB149	V1C	L	13PCW	91	F	European	2	6.39	10	5	YALE	6.216494	107.673951	15.065999
HSB149	HIP	L	13PCW	91	F	European	2	6.39	10	5	YALE	4.086294	86.535007	12.499033
HSB149	AMY	L	13PCW	91	F	European	2	6.39	10	5	YALE	7.056387	86.876744	17.5139
HSB149	STR	L	13PCW	91	F	European	2	6.39	10	5	YALE	6.153964	122.321897	17.526137
HSB149	MD	L	13PCW	91	F	European	2	6.39	10	5	YALE	2.360987	209.706035	24.244192
HSB149	CBC	L	13PCW	91	F	European	2	6.39	10	5	YALE	4.097269	104.163784	19.63736
HSB114	OFC	L	13PCW	91	M	European	1	NA	9.4	5	YALE	5.104712	117.625809	23.871032
HSB114	DFC	L	13PCW	91	M	European	1	NA	9.4	5	YALE	4.064324	140.086935	21.651434
HSB114	VFC	L	13PCW	91	M	European	1	NA	9.4	5	YALE	3.553341	137.531151	24.398319
HSB114	MFC	L	13PCW	91	M	European	1	NA	9.4	5	YALE	4.294422	140.611877	23.929095
HSB114	M1C	L	13PCW	91	M	European	1	NA	9.4	5	YALE	4.062283	131.828033	18.329112
HSB114	S1C	L	13PCW	91	M	European	1	NA	9.4	5	YALE	3.664195	133.66551	18.862614
HSB114	IPC	L	13PCW	91	M	European	1	NA	9.4	5	YALE	4.644189	123.469445	16.037024
HSB114	A1C	L	13PCW	91	M	European	1	NA	9.4	5	YALE	5.50325	87.569451	17.658724
HSB114	STC	L	13PCW	91	M	European	1	NA	9.4	5	YALE	5.148211	113.33257	19.255977
HSB114	ITC	L	13PCW	91	M	European	1	NA	9.4	5	YALE	5.765858	112.393186	15.964999
HSB114	V1C	L	13PCW	91	M	European	1	NA	9.4	5	YALE	6.309126	115.267655	12.087327
HSB114	HIP	L	13PCW	91	M	European	1	NA	9.4	5	YALE	2.750861	100.280704	11.719409
HSB114	AMY	L	13PCW	91	M	European	1	NA	9.4	5	YALE	5.781432	101.63797	13.579365
HSB114	STR	L	13PCW	91	M	European	1	NA	9.4	5	YALE	4.84066	142.215508	21.500307
HSB178	OFC	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.150668	151.577594	34.293141
HSB178	DFC	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.852826	149.709413	29.266833
HSB178	VFC	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.279327	157.539833	36.002427
HSB178	MFC	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	3.537519	129.181678	24.172027
HSB178	M1C	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.926565	146.716329	25.719117
HSB178	S1C	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.622537	142.759895	25.435101
HSB178	IPC	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	3.196963	140.086935	22.405292
HSB178	A1C	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	3.673292	132.739184	29.070584
HSB178	STC	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	3.909266	129.61394	24.553953
HSB178	ITC	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.896264	140.086935	23.266972
HSB178	V1C	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	5.894608	98.786647	11.322251
HSB178	HIP	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	1.94869	143.554151	15.334903
HSB178	AMY	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.878205	97.074745	13.562817
HSB178	STR	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.773479	164.880071	23.096238
HSB178	MD	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	1.818638	242.40497	25.546032
HSB178	CBC	L	16PCW	112	M	European	1	6.84	9.9	5	YALE	2.381383	69.741482	14.829206
HSB154	DFC	R	16PCW	112	M	African/European	1	6.44	10	5	USC	1.754169	137.532146	26.153699
HSB154	VFC	R	16PCW	112	M	African/European	1	6.44	10	5	USC	1.492665	162.457193	31.427562
HSB154	MFC	R	16PCW	112	M	African/European	1	6.44	10	5	USC	1.232446	153.272357	17.352897
HSB154	MSC	R	16PCW	112	M	African/European	1	6.44	10	5	USC	1.554095	167.270417	26.929878
HSB154	IPC	R	16PCW	112	M	African/European	1	6.44	10	5	USC	1.669927	150.503466	29.715362
HSB154	A1C	R	16PCW	112	M	African/European	1	6.44	10	5	USC	1.855043	140.611957	34.311121
HSB154	STC	R	16PCW	112	M	African/European	1	6.44	10	5	USC	1.78955	136.264777	30.359123
HSB154	ITC	R	16PCW	112	M	African/European	1	6.44	10	5	USC	2.217754	141.987645	26.207946
HSB154	V1C	R	16PCW	112	M	African/European	1	6.44	10	5	USC	2.391062	118.783363	23.335906
HSB154	HIP	R	16PCW	112	M	African/European	1	6.44	10	5	USC	6.123241	43.602737	11.439061
HSB154	AMY	R	16PCW	112	M	African/European	1	6.44	10	5	USC	2.01071	137.532146	19.855869
HSB154	STR	R	16PCW	112	M	African/European	1	6.44	10	5	USC	1.546151	161.148351	16.71495
HSB154	MD	R	16PCW	112	M	African/European	1	6.44	10	5	USC	2.744432	202.241999	17.211447
HSB96	DFC	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	1.972708	102.882979	20.143533

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB96	VFC	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	1.38154	143.863885	24.628536
HSB96	MFC	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	2.649983	82.200401	13.317262
HSB96	MSC	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	1.608421	142.215508	25.672903
HSB96	IPC	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	1.809163	138.539945	29.586584
HSB96	A1C	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	2.122961	140.086935	30.899769
HSB96	STC	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	2.22818	109.974629	18.265117
HSB96	V1C	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	2.928041	114.290524	20.760636
HSB96	HIP	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	0.578872	135.084367	9.35578
HSB96	STR	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	2.3472	159.657131	16.188317
HSB96	MD	R	16PCW	112	M	Mexican	2	NA	8.8	5	YALE	1.358775	180.49059	20.596399
HSB97	OFC	L	17PCW	119	F	European	2	NA	9.5	5	USC	0.848591	156.179378	30.876259
HSB97	DFC	L	17PCW	119	F	European	2	NA	9.5	5	USC	1.027685	166.559576	26.973489
HSB97	VFC	L	17PCW	119	F	European	2	NA	9.5	5	USC	0.85815	141.987645	26.253739
HSB97	MFC	L	17PCW	119	F	European	2	NA	9.5	5	USC	0.858663	157.994811	23.067623
HSB97	MSC	L	17PCW	119	F	European	2	NA	9.5	5	USC	0.963596	159.867088	25.606731
HSB97	IPC	L	17PCW	119	F	European	2	NA	9.5	5	USC	1.400336	152.707887	29.433934
HSB97	A1C	L	17PCW	119	F	European	2	NA	9.5	5	USC	1.336174	145.834239	30.702751
HSB97	STC	L	17PCW	119	F	European	2	NA	9.5	5	USC	1.130686	131.86367	25.423641
HSB97	V1C	L	17PCW	119	F	European	2	NA	9.5	5	USC	1.071888	122.447797	19.265463
HSB97	HIP	L	17PCW	119	F	European	2	NA	9.5	5	USC	0.347574	171.073453	13.141321
HSB97	AMY	L	17PCW	119	F	European	2	NA	9.5	5	USC	3.040604	90.440009	17.400362
HSB97	STR	L	17PCW	119	F	European	2	NA	9.5	5	USC	0.644331	152.707887	14.216526
HSB97	MD	L	17PCW	119	F	European	2	NA	9.5	5	USC	0.806202	187.334724	20.625169
HSB97	CBC	L	17PCW	119	F	European	2	NA	9.5	5	USC	1.351453	102.046199	17.591509
HSB98	DFC	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	0.723563	141.066662	29.203837
HSB98	VFC	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	0.864001	159.867088	25.808878
HSB98	MFC	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	0.698107	139.270344	19.556002
HSB98	MSC	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	0.820223	130.725721	35.789455
HSB98	IPC	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	0.98702	114.572234	41.227347
HSB98	A1C	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	0.953308	132.248675	33.515347
HSB98	STC	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	0.912386	135.027149	32.759005
HSB98	V1C	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	1.066362	122.13145	36.805893
HSB98	HIP	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	0.18914	126.511541	14.518952
HSB98	STR	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	2.175305	129.61265	17.585147
HSB98	MD	R	19PCW	133	F	Mexican	2	NA	8.8	5	USC	1.09615	170.196815	24.538151
HSB107	OFC	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.45531	144.360226	26.395334
HSB107	DFC	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.618988	142.454032	27.656453
HSB107	VFC	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.490885	155.586369	27.834155
HSB107	MFC	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.577662	158.612441	24.702827
HSB107	M1C	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.593507	181.630194	27.866996
HSB107	S1C	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.728301	163.122269	27.642222
HSB107	IPC	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.759286	155.586369	31.847267
HSB107	A1C	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.843257	165.161711	33.796603
HSB107	STC	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.628923	174.8543	25.461259
HSB107	ITC	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.519411	158.612441	22.496952
HSB107	V1C	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.614674	132.248675	18.55174
HSB107	HIP	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.174947	167.270417	14.920385
HSB107	AMY	L	21PCW	147	F	European	20	6.61	9.6	5	USC	1.070841	114.304745	16.500266
HSB107	STR	L	21PCW	147	F	European	20	6.61	9.6	5	USC	1.592765	125.730226	14.221259
HSB107	MD	L	21PCW	147	F	European	20	6.61	9.6	5	USC	0.716984	167.270417	14.122427
HSB107	CBC	L	21PCW	147	F	European	20	6.61	9.6	5	USC	1.731551	96.853528	15.680462

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB92	OFC	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.307483	157.994811	33.377866
HSB92	DFC	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.507025	181.630194	27.900993
HSB92	VFC	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.373523	188.176586	34.335944
HSB92	MFC	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.444906	187.202243	32.181025
HSB92	M1C	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.28654	188.176586	27.818696
HSB92	S1C	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.330215	194.32641	25.904151
HSB92	IPC	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.405303	151.046723	26.453438
HSB92	STC	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.651266	175.664186	28.595321
HSB92	ITC	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.223249	131.481532	18.202019
HSB92	V1C	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.681843	168.716687	32.22296
HSB92	HIP	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.081457	161.266263	15.9742
HSB92	AMY	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.23991	144.360226	21.685982
HSB92	STR	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.365306	167.270417	13.617009
HSB92	MD	R	21PCW	147	M	African	4	6.65	9.1	5	USC	0.869114	77.499759	7.915952
HSB92	CBC	R	21PCW	147	M	African	4	6.65	9.1	5	USC	2.12147	79.767938	13.939831
HSB159	OFC	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.302585	180.49059	32.522342
HSB159	DFC	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.46111	171.391508	35.17769
HSB159	VFC	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.304906	193.154538	33.448268
HSB159	MFC	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.22792	171.391508	28.472076
HSB159	M1C	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.377444	159.657131	23.324971
HSB159	S1C	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.41475	175.795638	29.559149
HSB159	IPC	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.732506	161.845309	32.157059
HSB159	A1C	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.581471	175.795638	32.785345
HSB159	STC	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.588699	174.143963	28.792447
HSB159	ITC	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.477964	170.543	31.624659
HSB159	V1C	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.396793	154.158609	20.182605
HSB159	HIP	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.696783	141.383402	12.534884
HSB159	AMY	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.529693	62.086981	12.761413
HSB159	STR	L	22PCW	154	M	European	1	6.58	10	5	YALE	1.540876	137.151428	13.103593
HSB159	MD	L	22PCW	154	M	European	1	6.58	10	5	YALE	0.372412	182.903197	14.131577
HSB159	CBC	L	22PCW	154	M	European	1	6.58	10	5	YALE	1.224277	110.56784	12.892898
HSB155	OFC	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.102633	88.453109	13.301226
HSB155	DFC	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.067294	71.666494	9.378335
HSB155	VFC	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.072037	86.958538	18.082105
HSB155	MFC	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.273463	46.271627	3.648535
HSB155	M1C	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.118898	52.573543	6.574262
HSB155	S1C	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.349472	74.586845	12.638567
HSB155	IPC	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.09858	45.736202	4.082129
HSB155	ITC	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.051737	82.352264	15.156004
HSB155	HIP	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.62736	60.590866	5.893915
HSB155	AMY	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.291469	36.167709	4.007573
HSB155	STR	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.672698	19.822483	5.517204
HSB155	MD	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.622244	35.951385	4.664362
HSB155	CBC	R	35PCW	245	F	European	48	6.67	7.2	5	YALE	0.494122	56.076697	7.931364
HSB194	OFC	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.041781	108.523489	18.020502
HSB194	DFC	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.070644	128.327348	18.669269
HSB194	VFC	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.070082	113.33257	16.372127
HSB194	MFC	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.039495	107.394193	14.909251
HSB194	M1C	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.090498	73.981925	10.205915
HSB194	S1C	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.065866	83.044884	12.590515
HSB194	IPC	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.146438	113.33257	18.194611

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB194	A1C	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.063484	107.394193	16.689455
HSB194	STC	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.171298	118.320579	19.951419
HSB194	ITC	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.150018	125.4398	20.355636
HSB194	V1C	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.060213	95.046611	17.413436
HSB194	HIP	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.031423	45.957712	5.907369
HSB194	AMY	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.063962	59.734516	6.126825
HSB194	STR	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.073479	53.573426	3.656252
HSB194	MD	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.236713	34.960445	3.34586
HSB194	CBC	L	37PCW	259	M	European	20	6.12	8.3	5	YALE	0.055026	60.74664	9.662803
HSB121	OFC	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.006368	45.909578	5.631735
HSB121	DFC	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.022373	41.287026	6.654639
HSB121	VFC	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.012647	43.635002	6.11308
HSB121	MFC	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.014781	37.476461	5.034661
HSB121	M1C	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.017274	44.439748	4.599102
HSB121	S1C	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.021926	39.468226	6.308283
HSB121	IPC	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.023303	48.421208	6.41227
HSB121	A1C	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.020998	35.188462	4.933568
HSB121	STC	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.036728	43.286404	6.384937
HSB121	ITC	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.039964	48.962281	6.830393
HSB121	V1C	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.006368	26.787544	6.263897
HSB121	HIP	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.006368	53.633327	9.670572
HSB121	AMY	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.020543	32.709072	5.268768
HSB121	STR	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.006368	18.39068	3.687353
HSB121	MD	R	4M	388	M	European	9.5	6.26	9	5	YALE	0.004923	39.731231	2.833661
HSB132	OFC	L	4M	388	M	European	22	6.6	7.7	5	USC	0.008003	126.070912	8.970919
HSB132	DFC	L	4M	388	M	European	22	6.6	7.7	5	USC	0.011455	118.675901	10.38789
HSB132	VFC	L	4M	388	M	European	22	6.6	7.7	5	USC	0.012661	122.447797	10.062818
HSB132	MFC	L	4M	388	M	European	22	6.6	7.7	5	USC	0.011455	130.351978	9.876871
HSB132	M1C	L	4M	388	M	European	22	6.6	7.7	5	USC	0.007163	114.304745	9.085435
HSB132	S1C	L	4M	388	M	European	22	6.6	7.7	5	USC	0.014356	115.9337	8.925972
HSB132	IPC	L	4M	388	M	European	22	6.6	7.7	5	USC	0.011455	115.384246	8.423549
HSB132	A1C	L	4M	388	M	European	22	6.6	7.7	5	USC	0.013231	93.884153	8.937675
HSB132	STC	L	4M	388	M	European	22	6.6	7.7	5	USC	0.027367	120.580294	9.539147
HSB132	ITC	L	4M	388	M	European	22	6.6	7.7	5	USC	0.027858	119.078139	9.680093
HSB132	V1C	L	4M	388	M	European	22	6.6	7.7	5	USC	0.020506	119.973697	9.658148
HSB132	HIP	L	4M	388	M	European	22	6.6	7.7	5	USC	0.011455	84.89582	6.968261
HSB132	AMY	L	4M	388	M	European	22	6.6	7.7	5	USC	0.010188	84.204352	6.825136
HSB132	STR	L	4M	388	M	European	22	6.6	7.7	5	USC	0.01596	58.399213	3.013502
HSB132	MD	L	4M	388	M	European	22	6.6	7.7	5	USC	0.006192	94.957947	6.005718
HSB132	CBC	L	4M	388	M	European	22	6.6	7.7	5	USC	0.008787	58.995905	8.559966
HSB139	OFC	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.013743	100.372379	10.376959
HSB139	DFC	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.020998	135.799459	12.114945
HSB139	VFC	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.030971	107.491209	10.191869
HSB139	MFC	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.008908	120.464166	12.227983
HSB139	M1C	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.011489	92.065585	8.50957
HSB139	S1C	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.026494	111.471794	11.573531
HSB139	IPC	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.049501	118.671599	10.278468
HSB139	A1C	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.013743	89.909803	11.204799
HSB139	STC	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.019178	90.179947	10.565526
HSB139	ITC	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.082125	111.776961	13.042506
HSB139	V1C	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.016285	123.57802	12.524239

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB139	HIP	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.007323	55.04461	6.813121
HSB139	AMY	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.006368	75.327348	7.631385
HSB139	STR	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.017274	40.292204	3.469339
HSB139	MD	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.008908	104.781545	5.916255
HSB139	CBC	L	4M	388	M	African	20	6.7	8.8	5	YALE	0.007323	73.530602	9.707269
HSB131	OFC	L	6M	448	F	European	26	6.26	7	5	USC	0.011455	40.111807	8.966365
HSB131	DFC	L	6M	448	F	European	26	6.26	7	5	USC	0.010843	42.260953	11.106435
HSB131	VFC	L	6M	448	F	European	26	6.26	7	5	USC	0.029324	47.342267	8.421427
HSB131	MFC	L	6M	448	F	European	26	6.26	7	5	USC	0.009514	42.721603	9.245956
HSB131	M1C	L	6M	448	F	European	26	6.26	7	5	USC	0.012661	43.430094	7.249009
HSB131	S1C	L	6M	448	F	European	26	6.26	7	5	USC	0.014895	36.044966	10.833447
HSB131	IPC	L	6M	448	F	European	26	6.26	7	5	USC	0.078668	43.747084	10.396562
HSB131	A1C	L	6M	448	F	European	26	6.26	7	5	USC	0.010843	36.54419	7.688422
HSB131	STC	L	6M	448	F	European	26	6.26	7	5	USC	0.051447	48.291415	11.984958
HSB131	ITC	L	6M	448	F	European	26	6.26	7	5	USC	0.049426	51.473772	16.446519
HSB131	V1C	L	6M	448	F	European	26	6.26	7	5	USC	0.012054	50.389135	18.309513
HSB131	HIP	L	6M	448	F	European	26	6.26	7	5	USC	0.025924	43.806644	7.443317
HSB131	AMY	L	6M	448	F	European	26	6.26	7	5	USC	0.008787	49.308266	10.167935
HSB131	STR	L	6M	448	F	European	26	6.26	7	5	USC	0.010188	23.976365	7.105242
HSB131	MD	L	6M	448	F	European	26	6.26	7	5	USC	0.016478	39.920416	6.385896
HSB131	CBC	L	6M	448	F	European	26	6.26	7	5	USC	0.013807	40.531593	7.237984
HSB171	OFC	L	301days	567	M	African	18	5.96	9.4	5	USC	0.029324	69.186517	7.366706
HSB171	DFC	L	301days	567	M	African	18	5.96	9.4	5	USC	0.021985	72.897361	7.694501
HSB171	VFC	L	301days	567	M	African	18	5.96	9.4	5	USC	0.024455	79.327815	7.845031
HSB171	MFC	L	301days	567	M	African	18	5.96	9.4	5	USC	0.019035	74.120494	8.297435
HSB171	S1C	L	301days	567	M	African	18	5.96	9.4	5	USC	0.008787	72.897361	7.135037
HSB171	IPC	L	301days	567	M	African	18	5.96	9.4	5	USC	0.018014	64.976721	7.094436
HSB171	STC	L	301days	567	M	African	18	5.96	9.4	5	USC	0.035572	66.098268	7.311708
HSB171	ITC	L	301days	567	M	African	18	5.96	9.4	5	USC	0.026866	72.897361	8.332271
HSB171	V1C	L	301days	567	M	African	18	5.96	9.4	5	USC	0.037514	77.727193	7.865179
HSB171	MD	L	301days	567	M	African	18	5.96	9.4	5	USC	0.029798	58.944667	6.525674
HSB171	CBC	L	301days	567	M	African	18	5.96	9.4	5	USC	0.007163	63.248741	10.028196
HSB122	OFC	R	12M	631	F	European	18	6.68	9	4	YALE	0.005377	85.033926	7.333525
HSB122	DFC	R	12M	631	F	European	18	6.68	9	4	YALE	0.004931	89.892575	8.230892
HSB122	VFC	R	12M	631	F	European	18	6.68	9	4	YALE	0.016795	83.906695	7.8836
HSB122	MFC	R	12M	631	F	European	18	6.68	9	4	YALE	0.017738	75.956985	7.767694
HSB122	M1C	R	12M	631	F	European	18	6.68	9	4	YALE	0.038118	81.239542	8.012522
HSB122	S1C	R	12M	631	F	European	18	6.68	9	4	YALE	0.014781	82.583231	8.269261
HSB122	IPC	R	12M	631	F	European	18	6.68	9	4	YALE	0.007323	91.123535	8.474032
HSB122	A1C	R	12M	631	F	European	18	6.68	9	4	YALE	0.008908	85.68021	8.436835
HSB122	STC	R	12M	631	F	European	18	6.68	9	4	YALE	0.007323	83.355885	8.290631
HSB122	ITC	R	12M	631	F	European	18	6.68	9	4	YALE	0.007323	91.399971	8.789406
HSB122	V1C	R	12M	631	F	European	18	6.68	9	4	YALE	0.008145	84.86631	8.856047
HSB122	HIP	R	12M	631	F	European	18	6.68	9	4	YALE	0.013743	66.64751	6.828605
HSB122	AMY	R	12M	631	F	European	18	6.68	9	4	YALE	0.006368	70.923041	6.887542
HSB122	STR	R	12M	631	F	European	18	6.68	9	4	YALE	0.007323	39.086245	2.771957
HSB122	MD	R	12M	631	F	European	18	6.68	9	4	YALE	0.007323	76.989055	5.952039
HSB122	CBC	R	12M	631	F	European	18	6.68	9	4	YALE	0.008145	66.287657	10.15297
HSB143	OFC	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.015444	46.236955	8.35185
HSB143	DFC	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.016478	30.788546	4.638739
HSB143	VFC	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.014895	31.492854	4.805498

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB143	MFC	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.012661	46.077656	6.90234
HSB143	M1C	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.01596	29.79449	4.205331
HSB143	S1C	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.029798	32.756029	3.457371
HSB143	IPC	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.011455	43.032263	5.939985
HSB143	A1C	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.034621	49.347667	7.942027
HSB143	STC	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.010843	33.885278	4.371088
HSB143	ITC	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.013807	45.342055	7.849039
HSB143	V1C	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.017016	39.193902	8.172615
HSB143	HIP	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.015444	30.702963	5.349472
HSB143	AMY	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.010843	40.36195	8.810844
HSB143	STR	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.009514	22.750577	3.448714
HSB143	MD	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.012661	38.912495	3.122318
HSB143	CBC	R	2Y	997	F	European	12	6.3	6.8	5	USC	0.014895	40.700414	6.344071
HSB173	VFC	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.009614	37.591899	4.188513
HSB173	M1C	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.009614	41.251481	4.486824
HSB173	S1C	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.010267	39.273609	4.33492
HSB173	IPC	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.007323	37.885386	4.786953
HSB173	A1C	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.014267	45.867789	4.535053
HSB173	STC	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.019633	47.083044	4.94242
HSB173	ITC	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.0109	45.097887	4.315792
HSB173	V1C	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.008908	44.647049	4.046294
HSB173	HIP	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.006368	43.247223	3.584834
HSB173	AMY	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.018701	35.708427	4.205783
HSB173	STR	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.015793	31.60223	2.249351
HSB173	MD	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.007323	53.629143	3.320275
HSB173	CBC	L	2Y178d	1175	F	European	8	6.03	8	5	YALE	0.015793	60.203075	6.469318
HSB172	OFC	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.004994	48.113154	4.718603
HSB172	DFC	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.006192	50.984249	3.821081
HSB172	VFC	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.008003	47.480891	4.035348
HSB172	MFC	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.007163	36.603198	3.965499
HSB172	M1C	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.009514	37.934731	3.449601
HSB172	S1C	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.025924	39.280968	4.009949
HSB172	IPC	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.008003	39.519642	3.658882
HSB172	A1C	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.008003	46.429386	3.980016
HSB172	STC	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.019541	43.949423	3.541569
HSB172	ITC	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.003784	41.888397	4.110632
HSB172	V1C	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.007163	40.824576	4.459434
HSB172	HIP	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.029798	38.865174	2.964551
HSB172	AMY	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.007163	38.798866	4.218646
HSB172	CBC	L	2Y305d	1302	M	Mexican	16	5.69	7.7	5	USC	0.008003	73.114579	6.968261
HSB118	OFC	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.022945	62.667896	4.60759
HSB118	DFC	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.018524	53.039914	4.502624
HSB118	VFC	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.009514	69.890107	5.396023
HSB118	MFC	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.014895	48.358878	4.856853
HSB118	M1C	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.016478	71.110527	4.526518
HSB118	S1C	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.021985	67.29781	5.457837
HSB118	IPC	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.013231	74.313364	6.184516
HSB118	A1C	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.012661	74.712859	5.818379
HSB118	STC	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.022945	45.976262	5.516166
HSB118	ITC	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.012054	75.414982	6.425146
HSB118	V1C	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.024947	44.593403	6.943632

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB118	HIP	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.007163	76.101445	5.06958
HSB118	AMY	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.008787	57.632637	5.396023
HSB118	STR	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.008003	44.593403	2.060486
HSB118	MD	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.006192	70.401594	4.018741
HSB118	CBC	R	4Y	1727	M	African	20	6.52	7.5	5	USC	0.010843	59.221541	4.222756
HSB141	OFC	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.031423	69.500801	4.646533
HSB141	DFC	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.00518	68.141201	4.884902
HSB141	VFC	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.022819	63.574377	4.411362
HSB141	MFC	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.051737	56.936361	4.727629
HSB141	M1C	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.077752	53.796111	4.822153
HSB141	S1C	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.060213	51.393816	4.614405
HSB141	IPC	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.012647	54.046949	4.682118
HSB141	A1C	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.012064	60.007135	3.64756
HSB141	STC	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.012647	60.082698	4.039016
HSB141	ITC	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.009614	59.052099	4.861479
HSB141	V1C	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.0109	48.469625	3.941058
HSB141	HIP	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.004564	64.006987	5.846468
HSB141	AMY	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.029629	57.287896	4.416985
HSB141	STR	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.007323	34.2178	2.414302
HSB141	MD	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.006368	66.009159	4.319251
HSB141	CBC	L	8Y	3188	M	African	30	6.54	8	5	YALE	0.010267	40.190956	5.027036
HSB174	OFC	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.007163	88.260956	6.070479
HSB174	DFC	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.146805	67.29781	3.813523
HSB174	VFC	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.012054	68.99257	3.637306
HSB174	MFC	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.904205	65.198138	3.925076
HSB174	IPC	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.02394	62.16597	3.725046
HSB174	A1C	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.016478	71.132579	4.327021
HSB174	STC	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.011455	71.302129	4.283345
HSB174	ITC	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.008003	65.590753	4.506992
HSB174	V1C	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.010843	57.212242	6.297588
HSB174	HIP	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.006192	67.190812	4.747031
HSB174	AMY	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.085701	68.309267	4.853335
HSB174	CBC	L	8Y90d	3278	M	African	16	6.25	8.9	5	USC	0.014895	60.634137	5.812737
HSB175	OFC	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.008908	64.762233	4.53389
HSB175	DFC	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.007323	68.781081	5.300704
HSB175	VFC	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.007323	70.459475	5.001644
HSB175	MFC	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.007323	77.918026	5.213292
HSB175	M1C	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.006368	62.937037	4.224362
HSB175	S1C	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.009614	64.405803	5.082134
HSB175	IPC	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.053572	61.942907	4.663143
HSB175	A1C	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.008908	75.956985	5.457867
HSB175	STC	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.044022	62.9582	4.483474
HSB175	ITC	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.013743	57.903311	5.361197
HSB175	V1C	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.006368	63.106077	4.597975
HSB175	HIP	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.044022	53.265123	5.126031
HSB175	AMY	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.008145	70.100362	5.640279
HSB175	CBC	L	10Y265d	4184	F	African	22	6.7	8.9	5	YALE	0.008908	57.219154	5.440078
HSB124	OFC	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.005528	77.740683	4.970213
HSB124	DFC	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.006368	76.83794	5.037169
HSB124	VFC	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.004949	76.157862	4.477614
HSB124	MFC	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.006368	70.100362	4.745781

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB124	M1C	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.014267	74.854067	5.290018
HSB124	S1C	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.005337	69.364389	5.307395
HSB124	IPC	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.008145	72.441847	4.672492
HSB124	A1C	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.016285	71.876727	4.213409
HSB124	STC	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.004669	81.676952	5.26332
HSB124	ITC	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.005007	78.535531	4.721562
HSB124	V1C	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.005038	59.961154	3.437448
HSB124	HIP	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.007323	46.138045	4.828312
HSB124	AMY	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.012064	63.317825	4.2829
HSB124	STR	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.006368	38.438954	2.290331
HSB124	MD	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.020543	52.68592	3.172126
HSB124	CBC	R	13Y	5014	F	African	19.5	6.34	9.2	5	YALE	0.008908	59.840916	5.501997
HSB119	OFC	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.007163	83.95362	5.228314
HSB119	DFC	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.008003	83.457469	5.46712
HSB119	VFC	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.007163	80.170317	5.372705
HSB119	MFC	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.007163	75.577594	4.590966
HSB119	M1C	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.007163	73.476661	4.536367
HSB119	S1C	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.008003	69.10723	4.720857
HSB119	IPC	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.007163	81.239274	5.027184
HSB119	A1C	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.006192	77.138764	4.814781
HSB119	STC	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.008003	80.170317	5.079346
HSB119	ITC	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.006192	84.330391	5.220743
HSB119	V1C	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.007163	63.043297	5.130977
HSB119	AMY	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.007163	74.36506	4.598707
HSB119	STR	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.008003	44.040757	1.908759
HSB119	MD	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.007163	80.734641	4.804353
HSB119	CBC	L	15Y	5745	M	African	14.5	6.93	9.5	4	USC	0.008787	64.163587	5.953129
HSB105	OFC	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.008787	58.34605	4.922878
HSB105	DFC	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.011455	65.672535	5.275066
HSB105	VFC	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.007163	58.671195	5.309739
HSB105	MFC	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.008003	44.840242	4.799758
HSB105	M1C	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.008003	44.260505	3.867083
HSB105	S1C	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.009514	45.660355	3.19863
HSB105	IPC	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.008787	54.58503	5.881258
HSB105	A1C	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.021985	41.158502	4.036356
HSB105	STC	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.008787	45.886987	4.658847
HSB105	ITC	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.016478	47.30834	4.783648
HSB105	V1C	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.008787	48.220743	5.268818
HSB105	HIP	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.008003	42.503062	4.782492
HSB105	CBC	L	18Y	6841	M	European	28	6.21	7.8	5	USC	0.009514	53.48288	4.796316
HSB127	OFC	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.005102	82.054526	4.892355
HSB127	DFC	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.004802	77.591513	5.146623
HSB127	VFC	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.005271	70.528651	4.739779
HSB127	MFC	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.004707	86.358795	5.660126
HSB127	M1C	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.00478	71.80669	4.010697
HSB127	S1C	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.004833	69.054114	4.37193
HSB127	IPC	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.013192	77.211657	5.089881
HSB127	A1C	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.019178	72.414878	4.132435
HSB127	STC	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.006368	72.300856	4.903591
HSB127	ITC	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.005281	76.1772	4.10677
HSB127	V1C	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.005254	62.707305	5.100166

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB127	HIP	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.013743	67.909746	5.123428
HSB127	AMY	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.004557	75.121941	4.626231
HSB127	STR	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.02471	34.535881	2.183946
HSB127	MD	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.006368	77.475167	4.233124
HSB127	CBC	L	19Y	7206	F	European	9.5	5.91	9.2	5	YALE	0.008908	62.916062	5.369406
HSB130	OFC	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.009614	59.393208	5.968639
HSB130	DFC	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.010267	57.20912	5.670118
HSB130	VFC	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.011489	53.168142	5.36531
HSB130	MFC	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.008908	49.82915	5.171412
HSB130	M1C	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.008908	52.102954	5.661556
HSB130	S1C	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.026951	52.110541	5.514421
HSB130	IPC	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.037185	54.849446	4.93984
HSB130	A1C	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.009614	55.362805	5.611973
HSB130	STC	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.009614	57.453314	5.035931
HSB130	ITC	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.010267	58.675287	5.704396
HSB130	V1C	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.008908	51.668478	5.315433
HSB130	HIP	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.017274	49.218828	5.479896
HSB130	AMY	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.009614	56.8498	4.607365
HSB130	STR	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.012064	38.683188	1.773284
HSB130	MD	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.008908	55.704879	4.409037
HSB130	CBC	L	21Y	7936	F	European	18	6.81	8.2	4	YALE	0.010267	49.022016	6.402651
HSB136	OFC	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.006192	63.691672	4.008988
HSB136	DFC	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.012054	60.768598	4.820583
HSB136	VFC	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.007163	68.853108	4.181974
HSB136	MFC	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.007163	63.955287	4.304169
HSB136	M1C	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.006192	62.098267	4.650999
HSB136	S1C	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.006192	66.085949	4.149765
HSB136	IPC	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.008003	58.507637	4.390121
HSB136	A1C	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.008003	59.110443	3.875727
HSB136	STC	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.006192	65.38111	3.644584
HSB136	ITC	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.007163	62.598259	4.384766
HSB136	V1C	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.006192	48.864351	3.307311
HSB136	HIP	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.006192	51.806343	3.894527
HSB136	AMY	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.004017	46.138073	3.926063
HSB136	STR	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.006192	38.640673	1.912328
HSB136	MD	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.007163	47.374832	2.720664
HSB136	CBC	R	23Y	8667	M	African	10.5	6.36	9	5	USC	0.042994	58.616215	5.410375
HSB126	OFC	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.006368	75.546103	4.928515
HSB126	DFC	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.006368	81.232102	4.759084
HSB126	VFC	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.019178	71.361863	3.853939
HSB126	MFC	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.005299	81.232102	5.238299
HSB126	M1C	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.008145	71.694913	4.976462
HSB126	S1C	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.008145	69.746198	4.878776
HSB126	IPC	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.007323	78.474336	4.984017
HSB126	A1C	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.010267	72.582673	3.696279
HSB126	STC	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.005184	73.178557	5.193616
HSB126	ITC	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.006368	80.511859	4.850426
HSB126	V1C	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.006368	59.644925	4.613238
HSB126	HIP	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.006368	66.081962	4.253025
HSB126	AMY	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.004948	68.916766	4.682118
HSB126	STR	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.005086	46.586986	1.904782

												mRNA expression (RPKM)		
Brain Code	Region Code	Hemisphere	Age	Days	Sex	Ethnicity	PMI	pH	RIN	Dissection Score	Sequencing Site	*IGF2BP1*	*MAPT*	*DAAM1*
HSB126	MD	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.006368	68.510071	4.342721
HSB126	CBC	R	30Y	11224	F	European	9.5	6.92	8.7	5	YALE	0.007323	68.241334	6.637674
HSB145	OFC	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.006368	71.280707	5.735972
HSB145	DFC	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.006368	62.979206	6.176367
HSB145	VFC	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.007323	61.307572	5.756201
HSB145	MFC	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.0109	69.192441	6.556032
HSB145	M1C	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.006368	62.770111	5.871608
HSB145	S1C	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.007323	68.984548	5.931124
HSB145	IPC	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.020998	68.678796	6.422097
HSB145	A1C	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.006368	61.440422	5.510272
HSB145	STC	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.010267	66.203573	5.114432
HSB145	ITC	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.005391	63.44711	4.838004
HSB145	V1C	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.007323	65.435168	5.492304
HSB145	HIP	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.006368	52.68592	4.695329
HSB145	AMY	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.015303	59.467329	5.171412
HSB145	STR	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.008145	34.288868	2.374714
HSB145	MD	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.006368	55.355896	3.97728
HSB145	CBC	R	36Y	13415	M	European	18	NA	8.3	5	YALE	0.010267	54.662035	5.381481
HSB123	OFC	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.006368	68.882301	4.672492
HSB123	DFC	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.008908	71.14171	4.617935
HSB123	VFC	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.006368	66.779478	5.091138
HSB123	MFC	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.008145	79.086548	6.703634
HSB123	M1C	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.007323	64.047625	5.518592
HSB123	S1C	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.007323	66.269317	5.83177
HSB123	IPC	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.006368	69.328771	4.966378
HSB123	A1C	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.007323	67.066667	4.973938
HSB123	STC	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.006368	66.454771	4.763998
HSB123	ITC	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.006368	72.688418	5.574039
HSB123	V1C	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.003602	69.600952	4.710795
HSB123	HIP	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.009614	75.598423	4.791771
HSB123	AMY	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.006368	67.453793	5.180601
HSB123	STR	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.007323	42.257562	2.198619
HSB123	MD	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.036298	71.501203	4.556999
HSB123	CBC	R	37Y	13780	M	African	13	6.37	8.2	5	YALE	0.05693	48.962281	4.309228
HSB135	OFC	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.007163	79.657366	5.028387
HSB135	DFC	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.038965	73.750984	4.099561
HSB135	VFC	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.016478	74.553405	5.033161
HSB135	M1C	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.015444	62.724686	4.751593
HSB135	S1C	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.011455	71.753532	5.253475
HSB135	IPC	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.009514	76.802773	5.188229
HSB135	A1C	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.014356	69.991114	5.468498
HSB135	STC	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.015444	75.221507	4.944258
HSB135	ITC	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.016478	76.002481	4.719734
HSB135	V1C	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.008003	65.183693	5.619968
HSB135	HIP	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.017016	48.975979	6.057431
HSB135	AMY	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.008787	47.342267	3.360649
HSB135	STR	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.007163	46.76259	2.082202
HSB135	MD	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.020506	59.334562	4.011913
HSB135	CBC	R	40Y	14876	F	African	30.5	6.82	9.2	4	USC	0.034621	46.172606	4.59759

Table E6. Over- or under-represented Gene Ontology biological process terms for the genes positively coexpressed with *IGF2BP1* across cortical regions in pren

The gene list analysis was carried out using the analysis tool in the PANTHER classification system (PMID: 25868073), with GO annotation data (PMID: 27899567). The GO terms were organized hierarchically, where the most post specific terms, indicated by bolded texts, were listed before the more general terms. The background gene set contains all 20,996 protein-coding genes available in PANTHER v.14.1. The test set contains 555 coding genes whose expression levels were positively correlated with *IGF2BP1* expression in all cortical regions in the prenatal brains. We used r ≥0.75 as the cut-off for positive-correlation coefficient, which was taken to be the 99th percentile of the empirical distribution of the correlation coefficients between *IGF2BP1* expression levels and the expression levels of all the other 60,153 coding and non-coding genes in neo-cortical regions of prenatal brains available in the BrainSpan database (http://www.brainspan.org/). The Pearson correlation coefficients were obtained using the vector of mRNA expression levels of each gene across all prenatal stages. For the regions that were not well parcellated during 8 – 10 post-conception weeks, their data were either merged (M1C and S1C) or used to represent the expression values in sub-regions (parietal cortex [PC] and temporal cortex [TC]).

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
positive regulation of G2/MI transition of meiotic cell cycle	3	3	0.08	36.84	+	3.46E-04	1.05E-02
positive regulation of meiotic cell cycle phase transition	5	3	0.14	22.10	+	9.31E-04	2.44E-02
positive regulation of cell cycle phase transition	95	24	2.58	9.31	+	7.01E-15	9.37E-13
regulation of cell cycle phase transition	450	73	12.22	5.98	+	5.38E-32	2.76E-29
regulation of cell cycle process	761	109	20.66	5.28	+	1.87E-43	2.29E-40
regulation of cell cycle	1190	140	32.31	4.33	+	2.55E-47	4.51E-44
regulation of cellular process	10941	387	297.03	1.30	+	4.93E-14	6.08E-12
regulation of biological process	11660	402	316.55	1.27	+	4.79E-13	5.36E-11
biological regulation	12352	422	335.33	1.26	+	9.74E-14	1.17E-11
positive regulation of cell cycle process	290	56	7.87	7.11	+	5.47E-28	2.12E-25
positive regulation of cell cycle	385	62	10.45	5.93	+	4.40E-27	1.49E-24
positive regulation of cellular process	5409	210	146.84	1.43	+	9.68E-09	6.16E-07
positive regulation of biological process	6166	220	167.39	1.31	+	3.16E-06	1.48E-04
regulation of meiotic cell cycle	50	8	1.36	5.89	+	1.36E-04	4.70E-03
regulation of meiotic cell cycle phase transition	8	4	0.22	18.42	+	2.02E-04	6.54E-03
positive regulation of cell cycle G2/M phase transition	30	11	0.81	13.51	+	6.15E-09	4.01E-07
regulation of cell cycle G2/M phase transition	211	35	5.73	6.11	+	4.38E-16	6.76E-14
regulation of G2/MI transition of meiotic cell cycle	3	3	0.08	36.84	+	3.46E-04	1.05E-02
DNA replication preinitiation complex assembly	**3**	**3**	**0.08**	**36.84**	**+**	**3.46E-04**	**1.05E-02**
cell cycle process	979	174	26.58	6.55	+	6.19E-85	4.92E-81
cellular process	14514	499	394.03	1.27	+	2.47E-24	6.67E-22
cell cycle	1323	212	35.92	5.90	+	2.77E-98	4.40E-94
nuclear DNA replication	44	24	1.19	20.09	+	4.26E-21	9.03E-19

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
cell cycle DNA replication	45	24	1.22	19.65	+	6.37E-21	1.33E-18
DNA-dependent DNA replication	119	40	3.23	12.38	+	6.98E-28	2.64E-25
DNA replication	211	64	5.73	11.17	+	7.14E-42	6.68E-39
cellular macromolecule biosynthetic process	1716	115	46.59	2.47	+	1.05E-18	1.95E-16
macromolecule biosynthetic process	1768	117	48	2.44	+	1.46E-18	2.67E-16
macromolecule metabolic process	6181	277	167.8	1.65	+	3.42E-21	7.45E-19
organic substance metabolic process	7853	306	213.19	1.44	+	8.06E-15	1.05E-12
metabolic process	8396	316	227.93	1.39	+	2.48E-13	2.92E-11
organic substance biosynthetic process	2862	147	77.7	1.89	+	3.35E-14	4.23E-12
biosynthetic process	2938	147	79.76	1.84	+	2.64E-13	3.06E-11
cellular biosynthetic process	2764	143	75.04	1.91	+	5.70E-14	6.92E-12
cellular metabolic process	7663	306	208.04	1.47	+	2.15E-16	3.45E-14
cellular macromolecule metabolic process	5088	252	138.13	1.82	+	1.49E-24	4.09E-22
protein-DNA complex assembly	200	54	5.43	9.95	+	3.00E-33	1.65E-30
cellular protein-containing complex assembly	838	72	22.75	3.16	+	7.23E-17	1.20E-14
protein-containing complex assembly	1566	102	42.51	2.40	+	9.46E-16	1.41E-13
cellular component assembly	2528	151	68.63	2.20	+	4.10E-20	8.26E-18
cellular component organization	5658	299	153.6	1.95	+	1.12E-36	7.40E-34
cellular component organization or biogenesis	5850	300	158.82	1.89	+	1.78E-34	1.09E-31
cellular component biogenesis	2758	157	74.87	2.10	+	3.42E-19	6.56E-17
protein-containing complex subunit organization	1851	117	50.25	2.33	+	3.62E-17	6.12E-15
protein-DNA complex subunit organization	242	56	6.57	8.52	+	1.79E-31	8.63E-29
mitotic DNA replication initiation	4	4	0.11	36.84	+	3.11E-05	1.21E-03
mitotic cell cycle process	600	144	16.29	8.84	+	2.77E-84	1.47E-80
mitotic cell cycle	687	151	18.65	8.10	+	5.32E-84	2.12E-80
nuclear cell cycle DNA replication initiation	4	4	0.11	36.84	+	3.11E-05	1.22E-03
cell cycle DNA replication initiation	4	4	0.11	36.84	+	3.11E-05	1.21E-03
DNA replication initiation	32	15	0.87	17.27	+	6.16E-13	6.76E-11
DNA metabolic process	745	110	20.23	5.44	+	5.31E-45	7.68E-42
nucleic acid metabolic process	2277	158	61.82	2.56	+	7.71E-28	2.85E-25
nucleobase-containing compound metabolic process	2788	177	75.69	2.34	+	3.95E-27	1.37E-24
organic cyclic compound metabolic process	3243	185	88.04	2.10	+	2.92E-23	7.26E-21

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
cellular nitrogen compound metabolic process	3425	190	92.98	2.04	+	1.49E-22	3.44E-20
nitrogen compound metabolic process	7006	293	190.2	1.54	+	2.98E-18	5.33E-16
heterocycle metabolic process	2968	181	80.58	2.25	+	6.46E-26	2.02E-23
cellular aromatic compound metabolic process	3008	181	81.66	2.22	+	4.31E-25	1.25E-22
primary metabolic process	7495	297	203.47	1.46	+	4.23E-15	5.75E-13
mitotic DNA replication	11	10	0.3	33.49	+	4.18E-11	3.61E-09
pre-replicative complex assembly involved in nuclear cell cycle DN	**7**	**6**	**0.19**	**31.57**	**+**	**4.87E-07**	**2.48E-05**
pre-replicative complex assembly involved in cell cycle DNA replica	7	6	0.19	31.57	+	4.87E-07	2.49E-05
pre-replicative complex assembly	7	6	0.19	31.57	+	4.87E-07	2.47E-05
meiotic chromosome condensation	6	5	0.16	30.70	+	5.13E-06	2.33E-04
chromosome organization involved in meiotic cell cycle	66	15	1.79	8.37	+	2.92E-09	1.96E-07
chromosome organization	1056	163	28.67	5.69	+	5.09E-71	1.62E-67
organelle organization	3410	240	92.57	2.59	+	1.06E-46	1.69E-43
meiotic cell cycle process	166	35	4.51	7.77	+	6.13E-19	1.15E-16
meiotic cell cycle	223	44	6.05	7.27	+	1.63E-22	3.71E-20
reproductive process	1426	96	38.71	2.48	+	1.42E-15	2.08E-13
reproduction	1429	97	38.79	2.50	+	4.28E-16	6.68E-14
chromosome condensation	43	19	1.17	16.28	+	1.16E-15	1.71E-13
DNA packaging	177	55	4.81	11.45	+	1.63E-36	1.04E-33
DNA conformation change	294	75	7.98	9.40	+	1.47E-44	1.95E-41
double-strand break repair via break-induced replication	**11**	**9**	**0.3**	**30.14**	**+**	**7.66E-10**	**5.69E-08**
double-strand break repair via homologous recombination	97	33	2.63	12.53	+	2.43E-23	6.13E-21
recombinational repair	98	33	2.66	12.40	+	3.17E-23	7.75E-21
DNA repair	512	86	13.9	6.19	+	9.90E-39	7.16E-36
cellular response to DNA damage stimulus	778	107	21.12	5.07	+	3.66E-41	3.24E-38
cellular response to stress	1704	136	46.26	2.94	+	3.58E-29	1.50E-26
cellular response to stimulus	6637	245	180.18	1.36	+	2.38E-08	1.45E-06
response to stimulus	8428	276	228.8	1.21	+	8.07E-05	2.87E-03
response to stress	3535	164	95.97	1.71	+	3.73E-12	3.69E-10
DNA recombination	221	47	6	7.83	+	3.47E-25	1.02E-22
double-strand break repair	181	44	4.91	8.95	+	1.15E-25	3.51E-23
mitochondrial DNA repair	5	4	0.14	29.47	+	5.47E-05	2.01E-03

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
mitochondrial DNA metabolic process	9	4	0.24	16.37	+	2.85E-04	8.85E-03
lagging strand elongation	**4**	**3**	**0.11**	**27.63**	**+**	**5.94E-04**	**1.65E-02**
DNA strand elongation involved in DNA replication	17	11	0.46	23.83	+	5.71E-11	4.83E-09
DNA strand elongation	22	12	0.6	20.09	+	3.34E-11	2.95E-09
embryonic body morphogenesis	6	4	0.16	24.56	+	8.93E-05	3.14E-03
embryonic morphogenesis	569	35	15.45	2.27	+	1.49E-05	6.27E-04
embryo development	979	63	26.58	2.37	+	9.86E-10	7.06E-08
multicellular organism development	5012	181	136.07	1.33	+	2.35E-05	9.50E-04
anatomical structure development	5399	193	146.57	1.32	+	1.95E-05	8.10E-04
developmental process	5749	210	156.07	1.35	+	1.20E-06	5.89E-05
positive regulation of exit from mitosis	**6**	**4**	**0.16**	**24.56**	**+**	**8.93E-05**	**3.14E-03**
regulation of exit from mitosis	20	6	0.54	11.05	+	4.87E-05	1.82E-03
regulation of mitotic cell cycle phase transition	415	68	11.27	6.04	+	4.69E-30	2.02E-27
regulation of mitotic cell cycle	630	95	17.1	5.55	+	2.29E-39	1.82E-36
regulation of mitotic nuclear division	171	42	4.64	9.05	+	1.07E-24	2.99E-22
regulation of nuclear division	196	42	5.32	7.89	+	9.99E-23	2.37E-20
regulation of organelle organization	1284	83	34.86	2.38	+	1.32E-12	1.37E-10
regulation of cellular component organization	2455	113	66.65	1.70	+	4.02E-08	2.42E-06
positive regulation of mitotic cell cycle phase transition	78	21	2.12	9.92	+	1.20E-13	1.44E-11
positive regulation of mitotic cell cycle	151	33	4.1	8.05	+	2.48E-18	4.48E-16
positive regulation of mitotic nuclear division	55	13	1.49	8.71	+	2.22E-08	1.36E-06
positive regulation of nuclear division	68	13	1.85	7.04	+	1.94E-07	1.05E-05
positive regulation of organelle organization	623	33	16.91	1.95	+	4.47E-04	1.30E-02
mitotic prophase	15	10	0.41	24.56	+	3.52E-10	2.68E-08
prophase	15	10	0.41	24.56	+	3.52E-10	2.69E-08
M phase	170	51	4.62	11.05	+	2.69E-33	1.59E-30
cell cycle phase	267	71	7.25	9.80	+	3.35E-43	3.33E-40
biological phase	267	71	7.25	9.80	+	3.35E-43	3.80E-40
mitotic M phase	170	51	4.62	11.05	+	2.69E-33	1.53E-30
mitotic cell cycle phase	267	71	7.25	9.80	+	3.35E-43	3.55E-40
DNA replication-dependent nucleosome assembly	**10**	**6**	**0.27**	**22.10**	**+**	**2.12E-06**	**1.01E-04**
DNA replication-dependent nucleosome organization	10	6	0.27	22.10	+	2.12E-06	1.00E-04

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
nucleosome organization	157	41	4.26	9.62	+	5.32E-25	1.51E-22
chromatin organization	695	79	18.87	4.19	+	2.64E-25	7.93E-23
chromatin assembly or disassembly	154	45	4.18	10.76	+	4.45E-29	1.82E-26
nucleosome assembly	116	39	3.15	12.38	+	3.24E-27	1.15E-24
chromatin assembly	133	42	3.61	11.63	+	2.51E-28	1.00E-25
meiotic sister chromatid cohesion, centromeric	5	3	0.14	22.10	+	9.31E-04	2.44E-02
meiosis II	10	4	0.27	14.73	+	3.91E-04	1.16E-02
meiosis II cell cycle process	10	4	0.27	14.73	+	3.91E-04	1.16E-02
meiotic nuclear division	152	32	4.13	7.75	+	2.09E-17	3.58E-15
nuclear division	279	69	7.57	9.11	+	2.96E-40	2.48E-37
organelle fission	306	70	8.31	8.43	+	6.01E-39	4.56E-36
sister chromatid segregation	138	42	3.75	11.21	+	8.55E-28	3.09E-25
nuclear chromosome segregation	215	53	5.84	9.08	+	5.53E-31	2.59E-28
chromosome segregation	270	66	7.33	9.00	+	3.00E-38	2.07E-35
meiotic chromosome segregation	90	19	2.44	7.78	+	6.82E-11	5.68E-09
sister chromatid cohesion	49	10	1.33	7.52	+	3.01E-06	1.41E-04
mitotic spindle midzone assembly	**7**	**4**	**0.19**	**21.05**	**+**	**1.37E-04**	**4.74E-03**
spindle midzone assembly	10	4	0.27	14.73	+	3.91E-04	1.16E-02
microtubule-based process	653	70	17.73	3.95	+	3.71E-21	7.98E-19
spindle assembly	85	21	2.31	9.10	+	5.00E-13	5.56E-11
organelle assembly	735	49	19.95	2.46	+	3.67E-08	2.21E-06
spindle organization	141	35	3.83	9.14	+	6.71E-21	1.39E-18
microtubule cytoskeleton organization	463	61	12.57	4.85	+	1.42E-22	3.32E-20
cytoskeleton organization	1084	68	29.43	2.31	+	5.54E-10	4.16E-08
mitotic spindle assembly	36	14	0.98	14.32	+	2.71E-11	2.41E-09
mitotic spindle organization	74	26	2.01	12.94	+	6.07E-19	1.15E-16
microtubule cytoskeleton organization involved in mitosis	103	34	2.8	12.16	+	1.16E-23	3.03E-21
mitotic nuclear division	141	45	3.83	11.76	+	1.93E-30	8.53E-28
mitotic spindle elongation	8	5	0.22	23.02	+	1.37E-05	5.80E-04
mitotic sister chromatid segregation	105	37	2.85	12.98	+	1.80E-26	5.98E-24
spindle elongation	9	5	0.24	20.46	+	2.08E-05	8.58E-04
CENP-A containing nucleosome assembly	31	17	0.84	20.20	+	2.35E-15	3.37E-13

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
histone exchange	49	17	1.33	12.78	+	8.97E-13	9.45E-11
ATP-dependent chromatin remodeling	77	19	2.09	9.09	+	6.60E-12	6.36E-10
chromatin remodeling	166	24	4.51	5.33	+	2.43E-10	1.90E-08
DNA replication-independent nucleosome assembly	40	18	1.09	16.58	+	5.13E-15	6.91E-13
DNA replication-independent nucleosome organization	41	19	1.11	17.07	+	5.82E-16	8.81E-14
CENP-A containing chromatin organization	31	17	0.84	20.20	+	2.35E-15	3.34E-13
centromere complex assembly	38	18	1.03	17.45	+	2.54E-15	3.55E-13
chromatin remodeling at centromere	34	18	0.92	19.50	+	5.63E-16	8.62E-14
B cell lineage commitment	**6**	**3**	**0.16**	**18.42**	**+**	**1.37E-03**	**3.43E-02**
animal organ development	3188	124	86.55	1.43	+	4.51E-05	1.71E-03
system development	4413	157	119.8	1.31	+	2.68E-04	8.41E-03
immune system development	655	36	17.78	2.02	+	1.42E-04	4.83E-03
female meiosis I	8	4	0.22	18.42	+	2.02E-04	6.55E-03
cellular process involved in reproduction in multicellular organism	32	11	0.87	12.66	+	1.07E-08	6.76E-07
multicellular organism reproduction	353	27	9.58	2.82	+	3.65E-06	1.70E-04
female gamete generation	840	47	22.8	2.06	+	8.07E-06	3.57E-04
gamete generation	134	15	3.64	4.12	+	1.00E-05	4.34E-04
multicellular organismal reproductive process	691	41	18.76	2.19	+	9.29E-06	4.08E-04
sexual reproduction	826	46	22.42	2.05	+	1.14E-05	4.89E-04
multi-organism reproductive process	832	45	22.59	1.99	+	2.20E-05	8.93E-04
multi-organism process	995	53	27.01	1.96	+	6.57E-06	2.96E-04
meiosis I	2810	108	76.29	1.42	+	2.40E-04	7.60E-03
meiosis I cell cycle process	110	20	2.99	6.70	+	2.23E-10	1.77E-08
negative regulation of double-strand break repair via nonhomolo	**113**	**21**	**3.07**	**6.85**	**+**	**5.51E-11**	**4.69E-09**
regulation of double-strand break repair	6	3	0.16	18.42	+	1.37E-03	3.42E-02
regulation of DNA repair	78	17	2.12	8.03	+	4.50E-10	3.39E-08
regulation of DNA metabolic process	124	21	3.37	6.24	+	2.52E-10	1.95E-08
regulation of macromolecule metabolic process	352	40	9.56	4.19	+	3.03E-13	3.49E-11
regulation of metabolic process	6180	263	167.77	1.57	+	1.55E-16	2.54E-14
regulation of nucleobase-containing compound metabolic process	6707	273	182.08	1.50	+	7.06E-15	9.35E-13
regulation of cellular metabolic process	4080	199	110.76	1.80	+	1.45E-17	2.50E-15
regulation of primary metabolic process	6245	261	169.54	1.54	+	2.03E-15	2.94E-13

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
regulation of nitrogen compound metabolic process	6051	255	164.27	1.55	+	2.38E-15	3.35E-13
regulation of response to DNA damage stimulus	5868	252	159.3	1.58	+	3.97E-16	6.25E-14
regulation of cellular response to stress	218	29	5.92	4.90	+	2.01E-11	1.83E-09
regulation of response to stress	722	53	19.6	2.70	+	2.79E-10	2.16E-08
negative regulation of double-strand break repair	1494	66	40.56	1.63	+	1.48E-04	4.99E-03
negative regulation of DNA repair	31	6	0.84	7.13	+	3.84E-04	1.14E-02
negative regulation of response to DNA damage stimulus	33	6	0.9	6.70	+	5.16E-04	1.48E-02
negative regulation of biological process	81	10	2.2	4.55	+	1.45E-04	4.90E-03
negative regulation of cellular process	5276	210	143.23	1.47	+	1.19E-09	8.43E-08
negative regulation of DNA metabolic process	4701	201	127.62	1.57	+	5.51E-12	5.37E-10
negative regulation of macromolecule metabolic process	122	17	3.31	5.13	+	1.64E-07	8.99E-06
negative regulation of metabolic process	2644	125	71.78	1.74	+	1.13E-09	8.03E-08
negative regulation of nucleobase-containing compound metabolic	2890	131	78.46	1.67	+	4.77E-09	3.13E-07
negative regulation of cellular metabolic process	1433	84	38.9	2.16	+	1.14E-10	9.30E-09
negative regulation of nitrogen compound metabolic process	2546	124	69.12	1.79	+	2.49E-10	1.94E-08
positive regulation of attachment of spindle microtubules to kine	2346	113	63.69	1.77	+	3.00E-09	2.01E-07
regulation of attachment of spindle microtubules to kinetochore	6	3	0.16	18.42	+	1.37E-03	3.42E-02
regulation of chromosome segregation	13	6	0.35	17.00	+	6.72E-06	3.02E-04
positive regulation of chromosome segregation	107	32	2.9	11.02	+	2.92E-21	6.54E-19
DNA unwinding involved in DNA replication	**29**	**9**	**0.79**	**11.43**	**+**	**4.86E-07**	**2.50E-05**
DNA duplex unwinding	14	7	0.38	18.42	+	7.32E-07	3.66E-05
DNA geometric change	109	20	2.96	6.76	+	1.93E-10	1.55E-08
histone H3-K27 trimethylation	118	23	3.2	7.18	+	2.83E-12	2.88E-10
histone H3-K27 methylation	6	3	0.16	18.42	+	1.37E-03	3.41E-02
histone modification	11	4	0.3	13.39	+	5.23E-04	1.50E-02
covalent chromatin modification	363	22	9.85	2.23	+	9.93E-04	2.60E-02
macromolecule modification	374	24	10.15	2.36	+	1.89E-04	6.19E-03
cellular protein modification process	3326	122	90.29	1.35	+	6.10E-04	1.69E-02
protein modification process	3106	117	84.32	1.39	+	2.71E-04	8.48E-03
cellular protein metabolic process	3106	117	84.32	1.39	+	2.71E-04	8.46E-03
regulation of transcription involved in G1/S transition of mitotic c	**3730**	**134**	**101.26**	**1.32**	**+**	**7.11E-04**	**1.92E-02**
G1/S transition of mitotic cell cycle	28	14	0.76	18.42	+	1.86E-12	1.92E-10

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mitotic cell cycle phase transition	121	43	3.28	13.09	+	1.04E-30	4.71E-28
cell cycle phase transition	272	77	7.38	10.43	+	1.58E-48	3.14E-45
cell cycle G1/S phase transition	280	78	7.6	10.26	+	9.96E-49	2.26E-45
regulation of transcription, DNA-templated	122	44	3.31	13.28	+	1.27E-31	6.30E-29
regulation of cellular macromolecule biosynthetic process	3516	161	95.45	1.69	+	1.70E-11	1.56E-09
regulation of cellular biosynthetic process	3952	181	107.29	1.69	+	4.09E-13	4.61E-11
regulation of biosynthetic process	4216	186	114.46	1.63	+	4.75E-12	4.66E-10
regulation of macromolecule biosynthetic process	4296	188	116.63	1.61	+	6.72E-12	6.44E-10
regulation of gene expression	4082	185	110.82	1.67	+	5.29E-13	5.84E-11
regulation of nucleic acid-templated transcription	4495	197	122.03	1.61	+	1.13E-12	1.18E-10
regulation of RNA biosynthetic process	3574	164	97.03	1.69	+	7.32E-12	6.97E-10
regulation of RNA metabolic process	3579	164	97.16	1.69	+	1.07E-11	9.98E-10
female meiosis chromosome segregation	3826	176	103.87	1.69	+	7.12E-13	7.65E-11
mitotic chromosome condensation	**6**	**3**	**0.16**	**18.42**	**+**	**1.37E-03**	**3.40E-02**
positive regulation of DNA-dependent DNA replication	17	8	0.46	17.33	+	1.65E-07	9.02E-06
regulation of DNA-dependent DNA replication	13	6	0.35	17.00	+	6.72E-06	3.01E-04
regulation of DNA replication	55	16	1.49	10.72	+	3.84E-11	3.34E-09
positive regulation of DNA replication	109	23	2.96	7.77	+	6.74E-13	7.34E-11
positive regulation of macromolecule biosynthetic process	37	8	1	7.96	+	2.06E-05	8.55E-04
positive regulation of macromolecule metabolic process	1899	92	51.55	1.78	+	9.98E-08	5.67E-06
positive regulation of metabolic process	3343	141	90.76	1.55	+	9.37E-08	5.40E-06
positive regulation of biosynthetic process	3614	147	98.11	1.50	+	4.15E-07	2.15E-05
positive regulation of cellular biosynthetic process	2018	94	54.78	1.72	+	4.54E-07	2.34E-05
positive regulation of cellular metabolic process	1985	94	53.89	1.74	+	2.49E-07	1.33E-05
protein localization to kinetochore	**3314**	**138**	**89.97**	**1.53**	**+**	**2.98E-07**	**1.58E-05**
protein localization to chromosome, centromeric region	13	6	0.35	17.00	+	6.72E-06	3.00E-04
protein localization to chromosome	17	7	0.46	15.17	+	2.03E-06	9.71E-05
protein localization to organelle	63	19	1.71	11.11	+	3.27E-13	3.74E-11
cellular localization	748	43	20.31	2.12	+	7.93E-06	3.51E-04
telomere maintenance via semi-conservative replication	2453	101	66.59	1.52	+	3.19E-05	1.24E-03
telomere maintenance	25	11	0.68	16.21	+	1.32E-09	9.28E-08
telomere organization	98	22	2.66	8.27	+	7.33E-13	7.82E-11

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
anatomical structure homeostasis	101	23	2.74	8.39	+	1.69E-13	2.01E-11
cerebral cortex regionalization	**341**	**24**	**9.26**	**2.59**	**+**	**4.42E-05**	**1.69E-03**
regionalization	7	3	0.19	15.79	+	1.92E-03	4.51E-02
pattern specification process	334	22	9.07	2.43	+	2.87E-04	8.89E-03
cerebral cortex development	433	29	11.76	2.47	+	2.11E-05	8.66E-04
pallium development	118	12	3.2	3.75	+	1.76E-04	5.80E-03
telencephalon development	176	15	4.78	3.14	+	1.78E-04	5.87E-03
forebrain development	258	18	7	2.57	+	4.26E-04	1.25E-02
brain development	392	25	10.64	2.35	+	1.48E-04	4.99E-03
head development	742	36	20.14	1.79	+	1.27E-03	3.22E-02
nervous system development	786	37	21.34	1.73	+	1.75E-03	4.16E-02
inner cell mass cell proliferation	2351	92	63.83	1.44	+	4.72E-04	1.37E-02
cell population proliferation	14	6	0.38	15.79	+	9.38E-06	4.11E-04
blastocyst growth	554	38	15.04	2.53	+	6.11E-07	3.08E-05
developmental growth	19	6	0.52	11.63	+	3.83E-05	1.47E-03
growth	394	24	10.7	2.24	+	5.00E-04	1.44E-02
blastocyst development	399	24	10.83	2.22	+	5.46E-04	1.54E-02
in utero embryonic development	103	11	2.8	3.93	+	2.20E-04	7.02E-03
chordate embryonic development	381	26	10.34	2.51	+	5.17E-05	1.91E-03
embryo development ending in birth or egg hatching	636	43	17.27	2.49	+	1.38E-07	7.64E-06
negative regulation of DNA endoreduplication	**654**	**43**	**17.75**	**2.42**	**+**	**3.82E-07**	**1.98E-05**
negative regulation of DNA-dependent DNA replication	7	3	0.19	15.79	+	1.92E-03	4.50E-02
negative regulation of DNA replication	25	8	0.68	11.79	+	1.76E-06	8.47E-05
negative regulation of cellular macromolecule biosynthetic process	40	11	1.09	10.13	+	7.30E-08	4.24E-06
negative regulation of cellular biosynthetic process	1390	84	37.74	2.23	+	2.02E-11	1.84E-09
negative regulation of biosynthetic process	1525	90	41.4	2.17	+	1.36E-11	1.26E-09
negative regulation of macromolecule biosynthetic process	1550	91	42.08	2.16	+	1.18E-11	1.10E-09
negative regulation of cell cycle process	1471	89	39.93	2.23	+	5.80E-12	5.63E-10
negative regulation of cell cycle	331	54	8.99	6.01	+	6.40E-24	1.70E-21
regulation of DNA endoreduplication	579	69	15.72	4.39	+	3.38E-23	8.16E-21
double-strand break repair via synthesis-dependent strand annea	10	5	0.27	18.42	+	3.06E-05	1.20E-03
spindle assembly involved in meiosis	**7**	**3**	**0.19**	**15.79**	**+**	**1.92E-03**	**4.49E-02**

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
meiotic spindle organization	7	3	0.19	15.79	+	1.92E-03	4.49E-02
negative regulation of cytokinesis	14	4	0.38	10.52	+	1.10E-03	2.83E-02
regulation of cytokinesis	7	3	0.19	15.79	+	1.92E-03	4.48E-02
regulation of cell division	88	16	2.39	6.70	+	1.42E-08	8.99E-07
negative regulation of cell division	167	20	4.53	4.41	+	1.29E-07	7.18E-06
positive regulation of mitotic cell cycle spindle assembly checkpoi	**17**	**4**	**0.46**	**8.67**	**+**	**2.02E-03**	**4.64E-02**
regulation of mitotic cell cycle spindle assembly checkpoint	7	3	0.19	15.79	+	1.92E-03	4.47E-02
regulation of mitotic metaphase/anaphase transition	14	6	0.38	15.79	+	9.38E-06	4.10E-04
regulation of mitotic sister chromatid separation	55	20	1.49	13.39	+	4.14E-15	5.67E-13
regulation of chromosome separation	61	22	1.66	13.28	+	2.00E-16	3.24E-14
regulation of mitotic sister chromatid segregation	66	22	1.79	12.28	+	7.74E-16	1.16E-13
regulation of sister chromatid segregation	72	23	1.95	11.77	+	3.65E-16	5.81E-14
regulation of chromosome organization	84	26	2.28	11.40	+	8.06E-18	1.41E-15
regulation of metaphase/anaphase transition of cell cycle	351	43	9.53	4.51	+	3.49E-15	4.83E-13
regulation of mitotic spindle checkpoint	57	20	1.55	12.92	+	7.22E-15	9.49E-13
regulation of spindle checkpoint	14	6	0.38	15.79	+	9.38E-06	4.08E-04
regulation of cell cycle checkpoint	14	6	0.38	15.79	+	9.38E-06	4.09E-04
positive regulation of spindle checkpoint	32	10	0.87	11.51	+	1.06E-07	5.96E-06
maintenance of DNA repeat elements	7	3	0.19	15.79	+	1.92E-03	4.47E-02
establishment of protein localization to telomere	**7**	**3**	**0.19**	**15.79**	**+**	**1.92E-03**	**4.46E-02**
establishment of protein localization to chromosome	7	3	0.19	15.79	+	1.92E-03	4.46E-02
mitotic spindle assembly checkpoint	15	5	0.41	12.28	+	1.41E-04	4.83E-03
mitotic spindle checkpoint	26	11	0.71	15.58	+	1.83E-09	1.27E-07
spindle checkpoint	26	11	0.71	15.58	+	1.83E-09	1.26E-07
cell cycle checkpoint	26	11	0.71	15.58	+	1.83E-09	1.25E-07
mitotic cell cycle checkpoint	198	43	5.38	8.00	+	1.94E-23	4.97E-21
negative regulation of mitotic cell cycle	159	37	4.32	8.57	+	3.33E-21	7.35E-19
spindle assembly checkpoint	310	48	8.42	5.70	+	1.60E-20	3.26E-18
negative regulation of mitotic metaphase/anaphase transition	26	11	0.71	15.58	+	1.83E-09	1.26E-07
negative regulation of mitotic cell cycle phase transition	28	12	0.76	15.79	+	2.95E-10	2.26E-08
negative regulation of cell cycle phase transition	219	38	5.95	6.39	+	6.16E-18	1.09E-15
negative regulation of metaphase/anaphase transition of cell cycle	235	41	6.38	6.43	+	2.45E-19	4.76E-17

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
negative regulation of mitotic sister chromatid separation	29	12	0.79	15.24	+	4.07E-10	3.08E-08
negative regulation of mitotic sister chromatid segregation	31	13	0.84	15.45	+	6.57E-11	5.50E-09
negative regulation of mitotic nuclear division	34	13	0.92	14.08	+	1.66E-10	1.34E-08
negative regulation of nuclear division	44	14	1.19	11.72	+	2.41E-10	1.90E-08
negative regulation of organelle organization	53	14	1.44	9.73	+	1.87E-09	1.27E-07
negative regulation of cellular component organization	382	33	10.37	3.18	+	2.19E-08	1.35E-06
negative regulation of sister chromatid segregation	705	39	19.14	2.04	+	5.71E-05	2.09E-03
negative regulation of chromosome segregation	36	14	0.98	14.32	+	2.71E-11	2.42E-09
negative regulation of chromosome organization	37	14	1	13.94	+	3.65E-11	3.19E-09
negative regulation of chromosome separation	139	27	3.77	7.16	+	3.80E-14	4.76E-12
signal transduction involved in G2 DNA damage checkpoint	**32**	**13**	**0.87**	**14.96**	**+**	**9.02E-11**	**7.44E-09**
negative regulation of cell cycle G2/M phase transition	12	5	0.33	15.35	+	6.03E-05	2.20E-03
signal transduction involved in DNA damage checkpoint	101	12	2.74	4.38	+	4.52E-05	1.71E-03
DNA damage checkpoint	73	19	1.98	9.59	+	2.96E-12	2.98E-10
DNA integrity checkpoint	134	25	3.64	6.87	+	7.45E-13	7.90E-11
signal transduction in response to DNA damage	146	31	3.96	7.82	+	5.43E-17	9.09E-15
signal transduction involved in DNA integrity checkpoint	105	22	2.85	7.72	+	2.42E-12	2.49E-10
signal transduction involved in cell cycle checkpoint	73	19	1.98	9.59	+	2.96E-12	2.97E-10
G2 DNA damage checkpoint	74	19	2.01	9.46	+	3.64E-12	3.61E-10
replicative senescence	**29**	**7**	**0.79**	**8.89**	**+**	**3.72E-05**	**1.43E-03**
cell aging	12	5	0.33	15.35	+	6.03E-05	2.19E-03
aging	65	9	1.76	5.10	+	1.42E-04	4.82E-03
chromatin silencing at rDNA	**280**	**18**	**7.6**	**2.37**	**+**	**1.36E-03**	**3.42E-02**
chromatin silencing	12	5	0.33	15.35	+	6.03E-05	2.19E-03
negative regulation of gene expression, epigenetic	60	9	1.63	5.53	+	8.16E-05	2.90E-03
regulation of gene expression, epigenetic	81	13	2.2	5.91	+	1.14E-06	5.61E-05
negative regulation of gene expression	234	30	6.35	4.72	+	2.06E-11	1.86E-09
chromatin organization involved in negative regulation of transcrip	1716	92	46.59	1.97	+	8.57E-10	6.20E-08
chromatin organization involved in regulation of transcription	60	9	1.63	5.53	+	8.16E-05	2.89E-03
negative regulation of transcription, DNA-templated	70	10	1.9	5.26	+	4.81E-05	1.80E-03
negative regulation of nucleic acid-templated transcription	1192	68	32.36	2.10	+	1.98E-08	1.23E-06
negative regulation of RNA biosynthetic process	1244	72	33.77	2.13	+	4.22E-09	2.80E-07

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
negative regulation of RNA metabolic process	1246	72	33.83	2.13	+	4.41E-09	2.91E-07
gene silencing	1334	75	36.22	2.07	+	7.65E-09	4.97E-07
positive regulation of G2/M transition of mitotic cell cycle	**152**	**14**	**4.13**	**3.39**	**+**	**1.38E-04**	**4.74E-03**
regulation of G2/M transition of mitotic cell cycle	27	11	0.73	15.01	+	2.52E-09	1.70E-07
regulation of mitotic centrosome separation	**194**	**31**	**5.27**	**5.89**	**+**	**5.29E-14**	**6.48E-12**
regulation of centrosome cycle	10	4	0.27	14.73	+	3.91E-04	1.16E-02
regulation of microtubule cytoskeleton organization	59	11	1.6	6.87	+	2.11E-06	1.00E-04
regulation of microtubule-based process	196	22	5.32	4.13	+	8.66E-08	5.01E-06
regulation of cytoskeleton organization	230	22	6.24	3.52	+	1.06E-06	5.24E-05
nucleotide-excision repair, DNA gap filling	**545**	**29**	**14.8**	**1.96**	**+**	**8.60E-04**	**2.28E-02**
nucleotide-excision repair	23	9	0.62	14.41	+	9.63E-08	5.53E-06
negative regulation of cellular senescence	**108**	**17**	**2.93**	**5.80**	**+**	**3.37E-08**	**2.04E-06**
negative regulation of cell aging	19	7	0.52	13.57	+	3.69E-06	1.71E-04
regulation of developmental process	25	8	0.68	11.79	+	1.76E-06	8.49E-05
regulation of cell aging	2571	98	69.8	1.40	+	7.68E-04	2.06E-02
regulation of cellular senescence	49	9	1.33	6.77	+	1.98E-05	8.24E-04
mitotic G1 phase	**42**	**8**	**1.14**	**7.02**	**+**	**4.58E-05**	**1.73E-03**
mitotic interphase	19	7	0.52	13.57	+	3.69E-06	1.70E-04
interphase	77	14	2.09	6.70	+	1.14E-07	6.41E-06
G1 phase	77	14	2.09	6.70	+	1.14E-07	6.39E-06
attachment of mitotic spindle microtubules to kinetochore	**19**	**7**	**0.52**	**13.57**	**+**	**3.69E-06**	**1.70E-04**
attachment of spindle microtubules to kinetochore	11	4	0.3	13.39	+	5.23E-04	1.50E-02
mitotic metaphase plate congression	20	6	0.54	11.05	+	4.87E-05	1.81E-03
metaphase plate congression	43	13	1.17	11.14	+	1.79E-09	1.24E-07
establishment of chromosome localization	53	14	1.44	9.73	+	1.87E-09	1.27E-07
chromosome localization	72	17	1.95	8.70	+	1.54E-10	1.25E-08
organelle localization	73	18	1.98	9.08	+	2.40E-11	2.15E-09
establishment of organelle localization	578	45	15.69	2.87	+	1.23E-09	8.67E-08
tetrahydrofolate interconversion	**362**	**29**	**9.83**	**2.95**	**+**	**6.71E-07**	**3.37E-05**
tetrahydrofolate metabolic process	11	4	0.3	13.39	+	5.23E-04	1.50E-02
folic acid-containing compound metabolic process	19	5	0.52	9.69	+	3.55E-04	1.07E-02
pteridine-containing compound metabolic process	28	5	0.76	6.58	+	1.63E-03	3.95E-02

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one-carbon metabolic process	34	6	0.92	6.50	+	5.93E-04	1.66E-02
histone-serine phosphorylation	**27**	**5**	**0.73**	**6.82**	**+**	**1.41E-03**	**3.50E-02**
histone phosphorylation	11	4	0.3	13.39	+	5.23E-04	1.49E-02
protein phosphorylation	29	9	0.79	11.43	+	4.86E-07	2.49E-05
phosphorylation	957	46	25.98	1.77	+	3.63E-04	1.09E-02
phosphorus metabolic process	1298	59	35.24	1.67	+	1.57E-04	5.25E-03
peptidyl-serine phosphorylation	2169	83	58.88	1.41	+	1.74E-03	4.16E-02
peptidyl-serine modification	175	15	4.75	3.16	+	1.68E-04	5.60E-03
purine nucleobase biosynthetic process	**199**	**17**	**5.4**	**3.15**	**+**	**6.57E-05**	**2.37E-03**
nucleobase metabolic process	11	4	0.3	13.39	+	5.23E-04	1.49E-02
nucleobase biosynthetic process	37	9	1	8.96	+	2.72E-06	1.28E-04
organic cyclic compound biosynthetic process	19	7	0.52	13.57	+	3.69E-06	1.71E-04
heterocycle biosynthetic process	1315	77	35.7	2.16	+	6.80E-10	5.08E-08
cellular nitrogen compound biosynthetic process	1169	76	31.74	2.39	+	8.16E-12	7.68E-10
aromatic compound biosynthetic process	1643	84	44.6	1.88	+	4.65E-08	2.77E-06
nucleosome positioning	**1177**	**75**	**31.95**	**2.35**	**+**	**3.34E-11**	**2.94E-09**
negative regulation of chromatin silencing	**17**	**6**	**0.46**	**13.00**	**+**	**2.28E-05**	**9.25E-04**
positive regulation of transcription, DNA-templated	20	7	0.54	12.89	+	4.87E-06	2.21E-04
positive regulation of gene expression	1547	78	42	1.86	+	2.90E-07	1.54E-05
positive regulation of nucleic acid-templated transcription	1998	92	54.24	1.70	+	9.00E-07	4.47E-05
positive regulation of RNA biosynthetic process	1634	81	44.36	1.83	+	3.76E-07	1.97E-05
positive regulation of RNA metabolic process	1635	81	44.39	1.82	+	3.78E-07	1.98E-05
positive regulation of nucleobase-containing compound metabolic	1719	85	46.67	1.82	+	1.43E-07	7.89E-06
positive regulation of nitrogen compound metabolic process	1881	94	51.07	1.84	+	2.29E-08	1.40E-06
negative regulation of gene silencing	3173	134	86.14	1.56	+	2.47E-07	1.32E-05
regulation of gene silencing	36	9	0.98	9.21	+	2.24E-06	1.06E-04
regulation of chromatin silencing	127	25	3.45	7.25	+	2.61E-13	3.05E-11
regulation of chromatin organization	38	9	1.03	8.72	+	3.29E-06	1.53E-04
positive regulation of gene expression, epigenetic	191	16	5.19	3.09	+	1.32E-04	4.57E-03
negative regulation of chromatin organization	64	13	1.74	7.48	+	1.05E-07	5.93E-06
DNA damage response, signal transduction by p53 class mediator	**63**	**10**	**1.71**	**5.85**	**+**	**2.14E-05**	**8.73E-04**
DNA damage response, signal transduction by p53 class mediator	15	5	0.41	12.28	+	1.41E-04	4.84E-03

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signal transduction by p53 class mediator	81	18	2.2	8.19	+	1.05E-10	8.59E-09
DNA damage response, signal transduction resulting in transcriptio	121	21	3.28	6.39	+	1.69E-10	1.36E-08
mitotic nuclear envelope disassembly	**16**	**5**	**0.43**	**11.51**	**+**	**1.82E-04**	**5.97E-03**
nuclear envelope disassembly	12	4	0.33	12.28	+	6.82E-04	1.86E-02
membrane disassembly	16	4	0.43	9.21	+	1.67E-03	4.03E-02
regulation of helicase activity	**16**	**4**	**0.43**	**9.21**	**+**	**1.67E-03**	**4.02E-02**
regulation of catalytic activity	12	4	0.33	12.28	+	6.82E-04	1.86E-02
regulation of molecular function	2319	88	62.96	1.40	+	1.51E-03	3.71E-02
positive regulation of ubiquitin protein ligase activity	**2995**	**110**	**81.31**	**1.35**	**+**	**1.07E-03**	**2.77E-02**
regulation of ubiquitin protein ligase activity	12	4	0.33	12.28	+	6.82E-04	1.85E-02
regulation of ubiquitin-protein transferase activity	24	7	0.65	10.74	+	1.32E-05	5.61E-04
regulation of protein modification process	53	7	1.44	4.87	+	9.97E-04	2.60E-02
regulation of transferase activity	1835	75	49.82	1.51	+	5.52E-04	1.55E-02
deoxyribonucleotide biosynthetic process	**980**	**50**	**26.61**	**1.88**	**+**	**3.63E-05**	**1.40E-03**
nucleobase-containing compound biosynthetic process	15	5	0.41	12.28	+	1.41E-04	4.81E-03
deoxyribonucleotide metabolic process	1098	73	29.81	2.45	+	7.87E-12	7.45E-10
mismatch repair	**35**	**6**	**0.95**	**6.31**	**+**	**6.80E-04**	**1.85E-02**
DNA replication checkpoint	**34**	**11**	**0.92**	**11.92**	**+**	**1.80E-08**	**1.12E-06**
DNA ligation	**16**	**5**	**0.43**	**11.51**	**+**	**1.82E-04**	**5.95E-03**
kinetochore assembly	**13**	**4**	**0.35**	**11.33**	**+**	**8.74E-04**	**2.32E-02**
kinetochore organization	13	4	0.35	11.33	+	8.74E-04	2.31E-02
positive regulation of chromatin binding	**18**	**9**	**0.49**	**18.42**	**+**	**1.81E-08**	**1.13E-06**
regulation of binding	13	4	0.35	11.33	+	8.74E-04	2.31E-02
regulation of chromatin binding	379	24	10.29	2.33	+	2.21E-04	7.02E-03
error-prone translesion synthesis	**23**	**5**	**0.62**	**8.01**	**+**	**7.53E-04**	**2.03E-02**
translesion synthesis	20	6	0.54	11.05	+	4.87E-05	1.81E-03
DNA synthesis involved in DNA repair	41	10	1.11	8.98	+	7.41E-07	3.69E-05
DNA biosynthetic process	51	11	1.38	7.94	+	5.99E-07	3.02E-05
postreplication repair	110	19	2.99	6.36	+	1.35E-09	9.43E-08
pyrimidine nucleobase metabolic process	**53**	**12**	**1.44**	**8.34**	**+**	**1.16E-07**	**6.50E-06**
mitotic prometaphase	**17**	**5**	**0.46**	**10.83**	**+**	**2.30E-04**	**7.30E-03**
protein localization to chromatin	**170**	**50**	**4.62**	**10.83**	**+**	**2.55E-32**	**1.35E-29**

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
negative regulation of G0 to G1 transition	**24**	**7**	**0.65**	**10.74**	**+**	**1.32E-05**	**5.62E-04**
regulation of G0 to G1 transition	39	11	1.06	10.39	+	5.86E-08	3.43E-06
DNA damage response, detection of DNA damage	**43**	**11**	**1.17**	**9.42**	**+**	**1.36E-07**	**7.57E-06**
determination of adult lifespan	**39**	**11**	**1.06**	**10.39**	**+**	**5.86E-08**	**3.42E-06**
interstrand cross-link repair	**18**	**5**	**0.49**	**10.23**	**+**	**2.87E-04**	**8.87E-03**
mitotic anaphase	**52**	**14**	**1.41**	**9.92**	**+**	**1.52E-09**	**1.06E-07**
anaphase	156	42	4.24	9.92	+	5.04E-26	1.60E-23
mitotic sister chromatid cohesion	**156**	**42**	**4.24**	**9.92**	**+**	**5.04E-26**	**1.63E-23**
V(D)J recombination	**15**	**4**	**0.41**	**9.82**	**+**	**1.36E-03**	**3.42E-02**
somatic diversification of immune receptors via germline recombir	15	4	0.41	9.82	+	1.36E-03	3.42E-02
somatic cell DNA recombination	34	9	0.92	9.75	+	1.49E-06	7.29E-05
somatic diversification of immune receptors	34	9	0.92	9.75	+	1.49E-06	7.27E-05
isotype switching	**47**	**9**	**1.28**	**7.05**	**+**	**1.48E-05**	**6.24E-04**
B cell activation involved in immune response	19	5	0.52	9.69	+	3.55E-04	1.07E-02
somatic recombination of immunoglobulin genes involved in immu	44	6	1.19	5.02	+	1.97E-03	4.56E-02
somatic recombination of immunoglobulin gene segments	19	5	0.52	9.69	+	3.55E-04	1.07E-02
somatic diversification of immunoglobulins	24	7	0.65	10.74	+	1.32E-05	5.59E-04
somatic diversification of immunoglobulins involved in immune res	36	7	0.98	7.16	+	1.22E-04	4.25E-03
immunoglobulin production involved in immunoglobulin mediated	19	5	0.52	9.69	+	3.55E-04	1.07E-02
base-excision repair	**27**	**5**	**0.73**	**6.82**	**+**	**1.41E-03**	**3.50E-02**
pyrimidine nucleoside biosynthetic process	**50**	**13**	**1.36**	**9.58**	**+**	**8.37E-09**	**5.39E-07**
pyrimidine-containing compound biosynthetic process	16	4	0.43	9.21	+	1.67E-03	4.04E-02
error-free translesion synthesis	**56**	**7**	**1.52**	**4.60**	**+**	**1.34E-03**	**3.37E-02**
pyrimidine nucleoside monophosphate biosynthetic process	**20**	**5**	**0.54**	**9.21**	**+**	**4.34E-04**	**1.27E-02**
nucleoside monophosphate biosynthetic process	16	4	0.43	9.21	+	1.67E-03	4.03E-02
nucleoside monophosphate metabolic process	45	7	1.22	5.73	+	4.14E-04	1.22E-02
pyrimidine nucleoside monophosphate metabolic process	73	8	1.98	4.04	+	1.34E-03	3.38E-02
G2/M transition of mitotic cell cycle	**17**	**4**	**0.46**	**8.67**	**+**	**2.02E-03**	**4.63E-02**
cell cycle G2/M phase transition	134	33	3.64	9.07	+	1.10E-19	2.18E-17
DNA damage response, signal transduction by p53 class mediator	**136**	**33**	**3.69**	**8.94**	**+**	**1.62E-19**	**3.18E-17**
signal transduction involved in mitotic G1 DNA damage checkpoint	58	14	1.57	8.89	+	5.06E-09	3.31E-07
intracellular signal transduction involved in G1 DNA damage check	59	15	1.6	9.36	+	7.74E-10	5.73E-08

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
negative regulation of cell cycle G1/S phase transition	59	15	1.6	9.36	+	7.74E-10	5.62E-08
regulation of cell cycle G1/S phase transition	109	23	2.96	7.77	+	6.74E-13	7.29E-11
G1 DNA damage checkpoint	170	30	4.62	6.50	+	1.35E-14	1.72E-12
mitotic G1 DNA damage checkpoint	67	17	1.82	9.35	+	5.86E-11	4.94E-09
mitotic G1/S transition checkpoint	66	17	1.79	9.49	+	4.79E-11	4.10E-09
negative regulation of G1/S transition of mitotic cell cycle	66	17	1.79	9.49	+	4.79E-11	4.12E-09
regulation of G1/S transition of mitotic cell cycle	106	23	2.88	7.99	+	4.07E-13	4.62E-11
mitotic DNA damage checkpoint	153	28	4.15	6.74	+	4.70E-14	5.84E-12
mitotic DNA integrity checkpoint	97	19	2.63	7.22	+	2.09E-10	1.66E-08
signal transduction involved in mitotic DNA damage checkpoint	106	22	2.88	7.65	+	2.85E-12	2.89E-10
signal transduction involved in mitotic DNA integrity checkpoint	59	15	1.6	9.36	+	7.74E-10	5.65E-08
signal transduction involved in mitotic cell cycle checkpoint	59	15	1.6	9.36	+	7.74E-10	5.68E-08
positive regulation of cell cycle arrest	59	15	1.6	9.36	+	7.74E-10	5.70E-08
regulation of cell cycle arrest	84	16	2.28	7.02	+	7.96E-09	5.15E-07
regulation of double-strand break repair via homologous recomb	**111**	**18**	**3.01**	**5.97**	**+**	**8.81E-09**	**5.65E-07**
regulation of DNA recombination	46	11	1.25	8.81	+	2.45E-07	1.32E-05
oocyte maturation	**102**	**20**	**2.77**	**7.22**	**+**	**6.85E-11**	**5.67E-09**
oocyte development	21	5	0.57	8.77	+	5.26E-04	1.49E-02
developmental process involved in reproduction	39	6	1.06	5.67	+	1.13E-03	2.88E-02
oocyte differentiation	668	38	18.13	2.10	+	3.67E-05	1.42E-03
microtubule depolymerization	**44**	**6**	**1.19**	**5.02**	**+**	**1.97E-03**	**4.55E-02**
regulation of nuclear cell cycle DNA replication	**17**	**4**	**0.46**	**8.67**	**+**	**2.02E-03**	**4.66E-02**
regulation of DNA damage checkpoint	**17**	**4**	**0.46**	**8.67**	**+**	**2.02E-03**	**4.65E-02**
serine family amino acid biosynthetic process	**17**	**4**	**0.46**	**8.67**	**+**	**2.02E-03**	**4.64E-02**
positive regulation of mitotic sister chromatid segregation	**17**	**4**	**0.46**	**8.67**	**+**	**2.02E-03**	**4.62E-02**
positive regulation of chromosome organization	17	4	0.46	8.67	+	2.02E-03	4.62E-02
protein localization to microtubule cytoskeleton	**175**	**14**	**4.75**	**2.95**	**+**	**5.24E-04**	**1.49E-02**
protein localization to cytoskeleton	34	8	0.92	8.67	+	1.21E-05	5.19E-04
establishment of mitotic spindle orientation	**39**	**8**	**1.06**	**7.56**	**+**	**2.87E-05**	**1.14E-03**
establishment of mitotic spindle localization	30	7	0.81	8.59	+	4.49E-05	1.70E-03
establishment of spindle localization	34	10	0.92	10.83	+	1.70E-07	9.22E-06
spindle localization	44	11	1.19	9.21	+	1.67E-07	9.07E-06

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
establishment of spindle orientation	49	12	1.33	9.02	+	5.54E-08	3.25E-06
establishment of cell polarity	36	8	0.98	8.19	+	1.74E-05	7.27E-04
establishment or maintenance of cell polarity	116	13	3.15	4.13	+	3.84E-05	1.47E-03
regulation of sister chromatid cohesion	**193**	**15**	**5.24**	**2.86**	**+**	**4.46E-04**	**1.30E-02**
chromosome separation	**22**	**5**	**0.6**	**8.37**	**+**	**6.32E-04**	**1.74E-02**
replication fork processing	**31**	**7**	**0.84**	**8.32**	**+**	**5.38E-05**	**1.98E-03**
DNA-dependent DNA replication maintenance of fidelity	31	7	0.84	8.32	+	5.38E-05	1.98E-03
negative regulation of DNA recombination	**40**	**9**	**1.09**	**8.29**	**+**	**4.73E-06**	**2.16E-04**
nucleotide-excision repair, DNA incision, 5'-to lesion	**45**	**10**	**1.22**	**8.19**	**+**	**1.54E-06**	**7.48E-05**
nucleotide-excision repair, DNA incision	37	8	1	7.96	+	2.06E-05	8.53E-04
nucleic acid phosphodiester bond hydrolysis	40	8	1.09	7.37	+	3.37E-05	1.31E-03
mitotic G2/M transition checkpoint	**299**	**22**	**8.12**	**2.71**	**+**	**4.94E-05**	**1.83E-03**
granulocyte differentiation	**28**	**6**	**0.76**	**7.89**	**+**	**2.38E-04**	**7.53E-03**
positive regulation of cytokinesis	**29**	**6**	**0.79**	**7.62**	**+**	**2.81E-04**	**8.75E-03**
positive regulation of cell division	39	8	1.06	7.56	+	2.87E-05	1.14E-03
cochlea morphogenesis	**87**	**9**	**2.36**	**3.81**	**+**	**9.96E-04**	**2.60E-02**
cochlea development	25	5	0.68	7.37	+	1.04E-03	2.70E-02
sensory organ development	53	7	1.44	4.87	+	9.97E-04	2.60E-02
embryonic organ morphogenesis	552	30	14.99	2.00	+	5.40E-04	1.53E-02
embryonic organ development	294	20	7.98	2.51	+	2.85E-04	8.86E-03
mitotic cytokinesis	**431**	**28**	**11.7**	**2.39**	**+**	**4.43E-05**	**1.69E-03**
cytoskeleton-dependent cytokinesis	71	14	1.93	7.26	+	4.69E-08	2.79E-06
cytokinesis	99	15	2.69	5.58	+	3.35E-07	1.76E-05
cell division	111	17	3.01	5.64	+	4.82E-08	2.84E-06
reciprocal meiotic recombination	**495**	**106**	**13.44**	**7.89**	**+**	**6.94E-57**	**1.84E-53**
homologous recombination	51	9	1.38	6.50	+	2.63E-05	1.05E-03
tRNA export from nucleus	**52**	**9**	**1.41**	**6.38**	**+**	**3.01E-05**	**1.19E-03**
tRNA-containing ribonucleoprotein complex export from nucleus	34	6	0.92	6.50	+	5.93E-04	1.66E-02
ribonucleoprotein complex export from nucleus	34	6	0.92	6.50	+	5.93E-04	1.66E-02
protein export from nucleus	126	11	3.42	3.22	+	1.05E-03	2.72E-02
nuclear export	150	12	4.07	2.95	+	1.28E-03	3.24E-02
nucleocytoplasmic transport	160	12	4.34	2.76	+	2.13E-03	4.86E-02

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
nuclear transport	264	18	7.17	2.51	+	5.50E-04	1.55E-02
transport	267	18	7.25	2.48	+	6.22E-04	1.72E-02
RNA export from nucleus	4521	84	122.74	0.68	-	6.32E-05	2.29E-03
RNA transport	129	11	3.5	3.14	+	1.26E-03	3.19E-02
establishment of RNA localization	197	14	5.35	2.62	+	1.53E-03	3.73E-02
RNA localization	199	15	5.4	2.78	+	6.00E-04	1.67E-02
nucleic acid transport	220	16	5.97	2.68	+	5.75E-04	1.61E-02
protein-containing complex localization	197	14	5.35	2.62	+	1.53E-03	3.72E-02
ribonucleoprotein complex localization	257	17	6.98	2.44	+	1.68E-03	4.03E-02
ncRNA export from nucleus	127	11	3.45	3.19	+	1.12E-03	2.87E-02
tRNA transport	38	6	1.03	5.82	+	9.98E-04	2.59E-02
response to X-ray	**36**	**6**	**0.98**	**6.14**	**+**	**7.76E-04**	**2.08E-02**
response to ionizing radiation	29	5	0.79	6.35	+	1.87E-03	4.42E-02
response to radiation	146	20	3.96	5.05	+	1.74E-08	1.09E-06
response to abiotic stimulus	439	36	11.92	3.02	+	1.73E-08	1.08E-06
centrosome duplication	**1161**	**57**	**31.52**	**1.81**	**+**	**2.90E-05**	**1.14E-03**
centrosome cycle	29	5	0.79	6.35	+	1.87E-03	4.41E-02
microtubule organizing center organization	82	17	2.23	7.64	+	8.78E-10	6.32E-08
nucleobase-containing small molecule interconversion	**92**	**17**	**2.5**	**6.81**	**+**	**4.06E-09**	**2.71E-07**
cellular response to gamma radiation	**29**	**5**	**0.79**	**6.35**	**+**	**1.87E-03**	**4.41E-02**
cellular response to ionizing radiation	30	5	0.81	6.14	+	2.14E-03	4.87E-02
cellular response to radiation	69	9	1.87	4.80	+	2.13E-04	6.83E-03
cellular response to abiotic stimulus	174	18	4.72	3.81	+	3.70E-06	1.70E-04
cellular response to environmental stimulus	312	19	8.47	2.24	+	1.52E-03	3.72E-02
response to gamma radiation	312	19	8.47	2.24	+	1.52E-03	3.72E-02
intrinsic apoptotic signaling pathway in response to DNA damage	**56**	**9**	**1.52**	**5.92**	**+**	**5.06E-05**	**1.87E-03**
intrinsic apoptotic signaling pathway in response to DNA damage	30	5	0.81	6.14	+	2.14E-03	4.86E-02
intrinsic apoptotic signaling pathway	71	11	1.93	5.71	+	1.02E-05	4.41E-04
apoptotic process	150	14	4.07	3.44	+	1.21E-04	4.22E-03
intrinsic apoptotic signaling pathway by p53 class mediator	904	43	24.54	1.75	+	5.66E-04	1.59E-02
regulation of gene silencing by miRNA	**51**	**7**	**1.38**	**5.06**	**+**	**8.13E-04**	**2.16E-02**
regulation of gene silencing by RNA	86	14	2.33	6.00	+	3.80E-07	1.98E-05

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
regulation of posttranscriptional gene silencing	89	15	2.42	6.21	+	9.76E-08	5.57E-06
cellular response to estradiol stimulus	**89**	**15**	**2.42**	**6.21**	**+**	**9.76E-08**	**5.59E-06**
cellular response to oxygen-containing compound	37	6	1	5.97	+	8.81E-04	2.33E-02
response to estradiol	1055	48	28.64	1.68	+	6.90E-04	1.87E-02
positive regulation of fibroblast proliferation	**139**	**11**	**3.77**	**2.92**	**+**	**2.18E-03**	**4.95E-02**
positive regulation of cell population proliferation	51	8	1.38	5.78	+	1.54E-04	5.15E-03
regulation of cell population proliferation	912	56	24.76	2.26	+	4.64E-08	2.77E-06
regulation of fibroblast proliferation	1611	85	43.74	1.94	+	8.88E-09	5.67E-07
homologous chromosome segregation	**82**	**12**	**2.23**	**5.39**	**+**	**6.88E-06**	**3.07E-04**
positive regulation of stem cell proliferation	**58**	**9**	**1.57**	**5.72**	**+**	**6.45E-05**	**2.33E-03**
regulation of stem cell proliferation	39	6	1.06	5.67	+	1.13E-03	2.89E-02
regulation of cyclin-dependent protein serine/threonine kinase a	**65**	**8**	**1.76**	**4.53**	**+**	**6.74E-04**	**1.85E-02**
regulation of cyclin-dependent protein kinase activity	99	15	2.69	5.58	+	3.35E-07	1.77E-05
regulation of protein kinase activity	103	15	2.8	5.36	+	5.27E-07	2.67E-05
regulation of kinase activity	788	39	21.39	1.82	+	5.27E-04	1.49E-02
regulation of phosphorylation	869	40	23.59	1.70	+	1.98E-03	4.58E-02
regulation of phosphate metabolic process	1585	66	43.03	1.53	+	7.52E-04	2.03E-02
regulation of phosphorus metabolic process	1779	76	48.3	1.57	+	1.39E-04	4.78E-03
regulation of protein serine/threonine kinase activity	1781	76	48.35	1.57	+	1.40E-04	4.81E-03
intracellular transport of virus	**507**	**30**	**13.76**	**2.18**	**+**	**1.67E-04**	**5.57E-03**
transport of virus	54	8	1.47	5.46	+	2.18E-04	6.98E-03
viral process	57	8	1.55	5.17	+	3.04E-04	9.36E-03
symbiotic process	700	38	19	2.00	+	9.39E-05	3.29E-03
interspecies interaction between organisms	782	40	21.23	1.88	+	2.15E-04	6.89E-03
multi-organism transport	826	43	22.42	1.92	+	8.37E-05	2.95E-03
multi-organism localization	70	10	1.9	5.26	+	4.81E-05	1.80E-03
anaphase-promoting complex-dependent catabolic process	**70**	**10**	**1.9**	**5.26**	**+**	**4.81E-05**	**1.81E-03**
regulation of spindle organization	**82**	**12**	**2.23**	**5.39**	**+**	**6.88E-06**	**3.06E-04**
regulation of centrosome duplication	**43**	**6**	**1.17**	**5.14**	**+**	**1.77E-03**	**4.21E-02**
regulation of cellular response to heat	**43**	**6**	**1.17**	**5.14**	**+**	**1.77E-03**	**4.21E-02**
transcription-coupled nucleotide-excision repair	**79**	**11**	**2.14**	**5.13**	**+**	**2.51E-05**	**1.01E-03**
animal organ regeneration	**73**	**10**	**1.98**	**5.05**	**+**	**6.62E-05**	**2.38E-03**

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
regeneration	74	10	2.01	4.98	+	7.34E-05	2.63E-03
positive regulation of neural precursor cell proliferation	**159**	**14**	**4.32**	**3.24**	**+**	**2.13E-04**	**6.83E-03**
regulation of neural precursor cell proliferation	52	7	1.41	4.96	+	9.01E-04	2.37E-02
neural tube closure	**90**	**10**	**2.44**	**4.09**	**+**	**3.16E-04**	**9.69E-03**
primary neural tube formation	93	12	2.52	4.75	+	2.16E-05	8.80E-04
neural tube formation	100	12	2.71	4.42	+	4.14E-05	1.58E-03
neural tube development	108	13	2.93	4.43	+	1.94E-05	8.10E-04
embryonic epithelial tube formation	162	15	4.4	3.41	+	7.61E-05	2.71E-03
morphogenesis of embryonic epithelium	126	13	3.42	3.80	+	8.35E-05	2.95E-03
epithelial tube formation	147	13	3.99	3.26	+	3.41E-04	1.04E-02
tube formation	134	13	3.64	3.57	+	1.48E-04	4.98E-03
tube closure	149	13	4.05	3.21	+	3.84E-04	1.15E-02
ciliary basal body-plasma membrane docking	**94**	**12**	**2.55**	**4.70**	**+**	**2.38E-05**	**9.59E-04**
organelle localization by membrane tethering	95	12	2.58	4.65	+	2.62E-05	1.05E-03
membrane docking	169	14	4.59	3.05	+	3.79E-04	1.13E-02
double-strand break repair via nonhomologous end joining	**178**	**14**	**4.83**	**2.90**	**+**	**6.13E-04**	**1.70E-02**
non-recombinational repair	56	7	1.52	4.60	+	1.34E-03	3.37E-02
mitotic S phase	**62**	**8**	**1.68**	**4.75**	**+**	**5.07E-04**	**1.46E-02**
S phase	65	8	1.76	4.53	+	6.74E-04	1.85E-02
smoothened signaling pathway	**65**	**8**	**1.76**	**4.53**	**+**	**6.74E-04**	**1.85E-02**
cellular response to fatty acid	**74**	**9**	**2.01**	**4.48**	**+**	**3.42E-04**	**1.04E-02**
cellular response to UV	**58**	**7**	**1.57**	**4.45**	**+**	**1.61E-03**	**3.91E-02**
response to UV	83	10	2.25	4.44	+	1.74E-04	5.74E-03
cellular response to light stimulus	144	17	3.91	4.35	+	1.35E-06	6.59E-05
regulation of signal transduction by p53 class mediator	**114**	**10**	**3.09**	**3.23**	**+**	**1.70E-03**	**4.07E-02**
positive regulation of DNA repair	**183**	**22**	**4.97**	**4.43**	**+**	**2.87E-08**	**1.74E-06**
positive regulation of DNA metabolic process	67	8	1.82	4.40	+	8.08E-04	2.15E-02
positive regulation of response to DNA damage stimulus	194	16	5.27	3.04	+	1.56E-04	5.22E-03
retrograde vesicle-mediated transport, Golgi to endoplasmic retic	**102**	**10**	**2.77**	**3.61**	**+**	**7.79E-04**	**2.08E-02**
vesicle-mediated transport	84	10	2.28	4.39	+	1.90E-04	6.20E-03
somite development	**1950**	**29**	**52.94**	**0.55**	**-**	**2.98E-04**	**9.19E-03**
mRNA export from nucleus	**82**	**9**	**2.23**	**4.04**	**+**	**6.76E-04**	**1.85E-02**

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
gene expression	109	11	2.96	3.72	+	3.45E-04	1.05E-02
mRNA transport	2011	79	54.59	1.45	+	1.19E-03	3.03E-02
mRNA-containing ribonucleoprotein complex export from nucleus	159	14	4.32	3.24	+	2.13E-04	6.85E-03
regulation of DNA binding	**109**	**11**	**2.96**	**3.72**	**+**	**3.45E-04**	**1.05E-02**
segmentation	**128**	**12**	**3.47**	**3.45**	**+**	**3.51E-04**	**1.06E-02**
antigen processing and presentation of exogenous peptide antige	**96**	**9**	**2.61**	**3.45**	**+**	**1.87E-03**	**4.41E-02**
regulation of ATP metabolic process	**98**	**9**	**2.66**	**3.38**	**+**	**2.14E-03**	**4.85E-02**
regulation of circadian rhythm	**121**	**11**	**3.28**	**3.35**	**+**	**7.74E-04**	**2.08E-02**
cellular response to oxidative stress	**114**	**10**	**3.09**	**3.23**	**+**	**1.70E-03**	**4.07E-02**
cellular response to hypoxia	**238**	**18**	**6.46**	**2.79**	**+**	**1.71E-04**	**5.67E-03**
cellular response to decreased oxygen levels	191	14	5.19	2.70	+	1.16E-03	2.96E-02
microtubule-based movement	**201**	**14**	**5.46**	**2.57**	**+**	**1.82E-03**	**4.30E-02**
anterior/posterior pattern specification	**269**	**19**	**7.3**	**2.60**	**+**	**2.58E-04**	**8.13E-03**
sex differentiation	**218**	**15**	**5.92**	**2.53**	**+**	**1.42E-03**	**3.51E-02**
negative regulation of transcription by RNA polymerase II	**268**	**18**	**7.28**	**2.47**	**+**	**6.48E-04**	**1.78E-02**
regulation of transcription by RNA polymerase II	857	52	23.27	2.24	+	2.07E-07	1.12E-05
gland development	**2699**	**121**	**73.27**	**1.65**	**+**	**4.77E-08**	**2.82E-06**
cellular response to drug	**414**	**24**	**11.24**	**2.14**	**+**	**7.65E-04**	**2.06E-02**
transcription by RNA polymerase II	**404**	**23**	**10.97**	**2.10**	**+**	**1.21E-03**	**3.07E-02**
transcription, DNA-templated	492	28	13.36	2.10	+	4.18E-04	1.23E-02
nucleic acid-templated transcription	650	38	17.65	2.15	+	2.73E-05	1.08E-03
RNA biosynthetic process	651	39	17.67	2.21	+	9.24E-06	4.07E-04
male gamete generation	**662**	**40**	**17.97**	**2.23**	**+**	**5.98E-06**	**2.70E-04**
protein modification by small protein conjugation	**559**	**30**	**15.18**	**1.98**	**+**	**6.14E-04**	**1.70E-02**
protein modification by small protein conjugation or removal	782	38	21.23	1.79	+	7.92E-04	2.11E-02
positive regulation of transcription by RNA polymerase II	**992**	**48**	**26.93**	**1.78**	**+**	**2.10E-04**	**6.78E-03**
secretion by cell	**1214**	**56**	**32.96**	**1.70**	**+**	**1.92E-04**	**6.24E-03**
export from cell	993	12	26.96	0.45	-	1.71E-03	4.10E-02
G protein-coupled receptor signaling pathway	**1032**	**12**	**28.02**	**0.43**	**-**	**1.01E-03**	**2.62E-02**
import into cell	**1302**	**15**	**35.35**	**0.42**	**-**	**1.73E-04**	**5.74E-03**
Unclassified	**675**	**6**	**18.32**	**0.33**	**-**	**1.47E-03**	**3.62E-02**
divalent inorganic cation homeostasis	**3181**	**27**	**86.36**	**0.31**	**-**	**8.94E-15**	**1.15E-12**

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
cation homeostasis	486	3	13.19	0.23	-	1.55E-03	3.78E-02
cellular metal ion homeostasis	**696**	**5**	**18.9**	**0.26**	**-**	**2.85E-04**	**8.87E-03**
metal ion homeostasis	552	3	14.99	0.20	-	4.05E-04	1.19E-02
cellular cation homeostasis	619	3	16.8	0.18	-	1.05E-04	3.67E-03
chemical synaptic transmission	**625**	**5**	**16.97**	**0.29**	**-**	**1.42E-03**	**3.51E-02**
anterograde trans-synaptic signaling	415	2	11.27	0.18	-	1.79E-03	4.24E-02
trans-synaptic signaling	415	2	11.27	0.18	-	1.79E-03	4.23E-02
metal ion transport	**433**	**2**	**11.76**	**0.17**	**-**	**1.27E-03**	**3.22E-02**
cation transport	634	3	17.21	0.17	-	7.42E-05	2.66E-03
ion transport	829	5	22.51	0.22	-	2.10E-05	8.63E-04
immune response-activating cell surface receptor signaling pathw	**1361**	**14**	**36.95**	**0.38**	**-**	**2.52E-05**	**1.01E-03**
immune response-regulating cell surface receptor signaling pathwa	447	2	12.14	0.16	-	8.91E-04	2.35E-02
regulation of immune response	482	2	13.09	0.15	-	4.50E-04	1.31E-02
inorganic cation transmembrane transport	**1134**	**12**	**30.79**	**0.39**	**-**	**1.94E-04**	**6.32E-03**
cation transmembrane transport	558	2	15.15	0.13	-	7.60E-05	2.72E-03
ion transmembrane transport	615	4	16.7	0.24	-	4.92E-04	1.42E-02
transmembrane transport	943	9	25.6	0.35	-	2.61E-04	8.21E-03
inorganic ion transmembrane transport	1285	12	34.89	0.34	-	1.00E-05	4.34E-04
regulation of ion transmembrane transporter activity	**642**	**4**	**17.43**	**0.23**	**-**	**2.50E-04**	**7.89E-03**
regulation of ion transmembrane transport	263	0	7.14	< 0.01	-	1.51E-03	3.71E-02
regulation of ion transport	485	2	13.17	0.15	-	4.61E-04	1.34E-02
regulation of transport	700	2	19	0.11	-	1.88E-06	9.05E-05
regulation of transmembrane transporter activity	1865	30	50.63	0.59	-	2.02E-03	4.66E-02
regulation of transporter activity	271	0	7.36	< 0.01	-	1.61E-03	3.91E-02
detection of chemical stimulus involved in sensory perception of	**283**	**0**	**7.68**	**< 0.01**	**-**	**1.06E-03**	**2.73E-02**
detection of chemical stimulus involved in sensory perception	430	0	11.67	< 0.01	-	2.13E-05	8.73E-04
sensory perception of chemical stimulus	480	0	13.03	< 0.01	-	4.09E-06	1.87E-04
sensory perception	532	1	14.44	0.07	-	1.45E-05	6.14E-04
nervous system process	960	11	26.06	0.42	-	1.39E-03	3.44E-02
system process	1380	19	37.46	0.51	-	1.01E-03	2.62E-02
detection of chemical stimulus	1958	22	53.16	0.41	-	1.02E-06	5.05E-05
detection of stimulus involved in sensory perception	517	0	14.04	< 0.01	-	2.00E-06	9.60E-05

GO BP complete	N REF (20,996)	N Set (555)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
sensory perception of smell	538	1	14.61	0.07	-	1.49E-05	6.27E-04
positive regulation of protein secretion	**460**	**1**	**12.49**	**0.08**	**-**	**9.58E-05**	**3.35E-03**
positive regulation of secretion	272	0	7.38	< 0.01	-	1.63E-03	3.95E-02
positive regulation of secretion by cell	435	1	11.81	0.08	-	2.07E-04	6.70E-03
positive regulation of secretion by cell	405	1	10.99	0.09	-	4.34E-04	1.27E-02

Table E7. Over- or under-represented Gene Ontology biological process terms for the genes positively coexpressed with *MAPT* across cortical regions in prenata

The gene list analysis was carried out using the analysis tool in the PANTHER classification system (PMID: 23868073), with GO annotation data (PMID: 27899567). The GO terms were organized hierarchically, where the most post specific terms, indicated by bolded texts, were listed before the more general terms. The background gene set contains all 20,996 protein-coding genes available in PANTHER v.14.1. The test set contains the 424 genes whose expression levels were positively correlated with *MAPT* expression in all cortical regions in the prenatal brains. We used r ≥0.66 as the cut-off for positive-correlation coefficient, which was taken to be the 99th percentile of the empirical distribution of the correlation coefficients between MAPT expression levels and the expression levels of all the other 60,153 coding and non-coding genes in neo-cortical regions of prenatal brains available in the BrainSpan database (http://www.brainspan.org/). The Pearson correlation coefficients were obtained using the vector of mRNA expression levels of each gene across all prenatal stages. For the regions that were not well parcellated during 8 – 10 post-conception weeks, their data were either merged (M1C and S1C) or used to represent the expression values in sub-regions (parietal cortex [PC] and temporal cortex [TC]).

GO BP complete	N REF (20,996)	N Set (424)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
receptor localization to synapse	**41**	**7**	**0.83**	**8.43**	**+**	**4.20E-05**	**1.48E-02**
localization	5662	153	114.61	1.33	+	5.50E-05	1.85E-02
cellular localization	2408	85	48.74	1.74	+	5.23E-07	1.65E-03
synaptic vesicle exocytosis	**63**	**9**	**1.28**	**7.06**	**+**	**1.23E-05**	**6.29E-03**
neurotransmitter secretion	100	11	2.02	5.43	+	1.32E-05	6.51E-03
establishment of localization in cell	1803	63	36.5	1.73	+	2.70E-05	1.12E-02
establishment of localization	4593	128	92.97	1.38	+	9.07E-05	2.65E-02
neurotransmitter transport	174	14	3.52	3.97	+	2.49E-05	1.09E-02
transport	4472	126	90.52	1.39	+	6.08E-05	2.00E-02
signal release from synapse	101	11	2.04	5.38	+	1.43E-05	6.67E-03
synaptic signaling	439	28	8.89	3.15	+	2.40E-07	1.27E-03
cell-cell signaling	1093	43	22.12	1.94	+	6.40E-05	2.02E-02
regulation of neurotransmitter levels	350	22	7.08	3.11	+	5.92E-06	3.90E-03
chemical synaptic transmission	411	26	8.32	3.13	+	7.54E-07	1.70E-03
anterograde trans-synaptic signaling	411	26	8.32	3.13	+	7.54E-07	1.49E-03
trans-synaptic signaling	429	27	8.68	3.11	+	5.06E-07	2.00E-03
synaptic vesicle transport	92	12	1.86	6.44	+	1.06E-06	1.68E-03
synaptic vesicle localization	97	12	1.96	6.11	+	1.76E-06	1.86E-03
vesicle localization	234	21	4.74	4.43	+	4.44E-08	7.03E-04
organelle localization	597	30	12.08	2.48	+	1.21E-05	6.38E-03
intracellular transport	1551	54	31.4	1.72	+	1.23E-04	3.37E-02
vesicle-mediated transport in synapse	132	13	2.67	4.87	+	6.64E-06	4.04E-03
establishment of synaptic vesicle localization	92	12	1.86	6.44	+	1.06E-06	1.53E-03
establishment of vesicle localization	224	20	4.53	4.41	+	1.01E-07	7.96E-04
establishment of organelle localization	400	22	8.1	2.72	+	4.13E-05	1.49E-02
calcium ion regulated exocytosis	78	11	1.58	6.97	+	1.50E-06	1.98E-03
axonal transport	**52**	**7**	**1.05**	**6.65**	**+**	**1.61E-04**	**3.99E-02**
microtubule-based movement	262	16	5.3	3.02	+	1.50E-04	3.83E-02

GO BP complete	N REF (20,996)	N Set (424)	expected	Fold Enrichment	over(+) or under(-) represenation	raw P	FDR
regulation of calcium ion-dependent exocytosis	**116**	**12**	**2.35**	**5.11**	**+**	**9.50E-06**	**5.18E-03**
regulation of regulated secretory pathway	163	13	3.3	3.94	+	5.24E-05	1.80E-02
regulation of exocytosis	219	17	4.43	3.83	+	5.35E-06	3.68E-03
regulation of transport	1829	68	37.02	1.84	+	1.61E-06	1.82E-03
regulation of localization	2702	88	54.69	1.61	+	7.88E-06	4.45E-03
regulation of secretion by cell	731	32	14.8	2.16	+	8.69E-05	2.59E-02
protein localization to cell periphery	**224**	**16**	**4.53**	**3.53**	**+**	**2.63E-05**	**1.13E-02**
regulation of synaptic plasticity	**183**	**13**	**3.7**	**3.51**	**+**	**1.56E-04**	**3.92E-02**
modulation of chemical synaptic transmission	438	26	8.87	2.93	+	2.29E-06	2.01E-03
regulation of trans-synaptic signaling	439	26	8.89	2.93	+	2.38E-06	1.89E-03
regulation of signaling	3674	109	74.37	1.47	+	3.57E-05	1.31E-02
regulation of axonogenesis	**187**	**13**	**3.79**	**3.43**	**+**	**1.90E-04**	**4.63E-02**
regulation of cell morphogenesis involved in differentiation	302	18	6.11	2.94	+	7.90E-05	2.40E-02
regulation of cell morphogenesis	483	25	9.78	2.56	+	3.26E-05	1.26E-02
regulation of cell development	928	39	18.78	2.08	+	2.72E-05	1.10E-02
regulation of neuron projection development	490	29	9.92	2.92	+	6.29E-07	1.66E-03
regulation of neuron differentiation	649	32	13.14	2.44	+	7.63E-06	4.47E-03
regulation of neurogenesis	807	33	16.34	2.02	+	2.01E-04	4.81E-02
regulation of nervous system development	914	37	18.5	2	+	1.08E-04	3.05E-02
generation of neurons	1513	58	30.63	1.89	+	4.79E-06	3.44E-03
neurogenesis	1612	61	32.63	1.87	+	3.76E-06	2.83E-03
nervous system development	2324	82	47.04	1.74	+	8.19E-07	1.44E-03
regulation of plasma membrane bounded cell projection organization	657	34	13.3	2.56	+	2.01E-06	1.99E-03
regulation of cell projection organization	666	34	13.48	2.52	+	2.30E-06	1.91E-03
regulation of membrane potential	**425**	**22**	**8.6**	**2.56**	**+**	**9.62E-05**	**2.77E-02**
neuron projection development	**659**	**31**	**13.34**	**2.32**	**+**	**3.44E-05**	**1.30E-02**
plasma membrane bounded cell projection organization	1082	47	21.9	2.15	+	1.57E-06	1.91E-03
cell projection organization	1122	48	22.71	2.11	+	2.20E-06	2.05E-03
neuron development	804	37	16.27	2.27	+	6.32E-06	4.00E-03
neuron differentiation	992	39	20.08	1.94	+	1.26E-04	3.37E-02
regulation of transcription by RNA polymerase II	**2694**	**27**	**54.53**	**0.5**	**-**	**2.42E-05**	**1.09E-02**
regulation of gene expression	4475	55	90.58	0.61	-	1.42E-05	6.80E-03
regulation of nucleic acid-templated transcription	3580	44	72.47	0.61	-	1.43E-04	3.76E-02
regulation of RNA biosynthetic process	3588	44	72.63	0.61	-	1.43E-04	3.71E-02
regulation of RNA metabolic process	3834	47	77.61	0.61	-	7.45E-05	2.31E-02
regulation of nucleobase-containing compound metabolic process	4080	52	82.59	0.63	-	1.12E-04	3.11E-02
nucleic acid metabolic process	**2263**	**21**	**45.81**	**0.46**	**-**	**3.25E-05**	**1.29E-02**
positive regulation of cell population proliferation	**934**	**4**	**18.91**	**0.21**	**-**	**6.21E-05**	**2.00E-02**

Table E8. Over- or under-represented Gene Ontology biological process terms for the genes positively coexpressed with *DAAM1* across cortical regions in pre

The gene list analysis was carried out using the analysis tool in the PANTHER classification system (PMID: 23868073), with GO annotation data (PMID: 27899567). The GO terms were organized *hierarchically*, where the most post specific terms, indicated by bolded texts, were listed before the more general terms. The background gene set contains all 21,042 protein-coding genes available in PANTHER 13.1 version. The test set contains the 339 genes whose expression levels were positively correlated with *DAAM1* expression in all cortical regions in the prenatal brains. We used r ≥0.56 as the cut-off for positive-correlation coefficient, which was taken to be the 99th percentile of the empirical distribution of the correlation coefficients between *DAAM1* expression levels and the expression levels of all the other 60,153 coding and non-coding genes in neo-cortical regions of prenatal brains available in the BrainSpan database (http://www.brainspan.org/). The Pearson correlation coefficients were obtained using the vector of mRNA expression levels of each gene across all prenatal stages. For the regions that were not well parcellated during 8 – 10 post-conception weeks, their data were either merged (M1C and S1C) or used to represent the expression values in sub-regions (parietal cortex [PC] and temporal cortex [TC]).

GO BP complete	N REF (21,042)	N Set (339)	expected	Fold Enrichment	over(+) or under(-) represenatio	raw P	FDR
membrane fission	**14**	**4**	**0.23**	**17.73**	**+**	**1.59E-04**	**3.15E-02**
cellular component organization	5584	135	89.96	1.5	+	1.64E-07	2.56E-04
cellular process	15478	280	249.36	1.12	+	1.10E-04	2.54E-02
cellular component organization or biogenesis	5773	138	93.01	1.48	+	2.21E-07	2.30E-04
clathrin-dependent endocytosis	**25**	**6**	**0.4**	**14.9**	**+**	**8.01E-06**	**3.48E-03**
localization	5608	123	90.35	1.36	+	1.20E-04	2.61E-02
positive regulation of dendritic spine morphogenesis	**17**	**4**	**0.27**	**14.6**	**+**	**3.00E-04**	**4.51E-02**
regulation of dendritic spine morphogenesis	37	7	0.6	11.74	+	5.48E-06	2.52E-03
regulation of dendrite morphogenesis	86	9	1.39	6.5	+	2.02E-05	7.35E-03
regulation of cell morphogenesis involved in differentiation	292	18	4.7	3.83	+	2.56E-06	1.60E-03
regulation of cell morphogenesis	488	25	7.86	3.18	+	7.74E-07	6.05E-04
regulation of cellular component organization	2434	73	39.21	1.86	+	2.26E-07	2.21E-04
biological regulation	12409	234	199.92	1.17	+	1.82E-04	3.52E-02
regulation of cell development	881	37	14.19	2.61	+	2.06E-07	2.30E-04
regulation of dendrite development	140	14	2.26	6.21	+	1.73E-07	2.26E-04
regulation of neuron projection development	466	31	7.51	4.13	+	9.76E-11	1.53E-06
regulation of neuron differentiation	623	34	10.04	3.39	+	1.60E-09	6.25E-06
regulation of neurogenesis	765	34	12.32	2.76	+	1.91E-07	2.30E-04
regulation of nervous system development	853	35	13.74	2.55	+	7.55E-07	6.22E-04
generation of neurons	1480	54	23.84	2.26	+	2.91E-08	5.69E-05
neurogenesis	1577	54	25.41	2.13	+	2.43E-07	2.23E-04
nervous system development	2298	76	37.02	2.05	+	1.64E-09	5.14E-06

GO BP complete	N REF (21,042)	N Set (339)	expected	Fold Enrichment	over(+) or under(-) represenatio	raw P	FDR
regulation of plasma membrane bounded cell projection organizatio	620	35	9.99	3.5	+	3.88E-10	3.03E-06
regulation of cell projection organization	629	35	10.13	3.45	+	5.57E-10	2.90E-06
regulation of postsynapse organization	58	7	0.93	7.49	+	7.49E-05	1.92E-02
regulation of dendritic spine development	68	9	1.1	8.22	+	3.56E-06	2.06E-03
positive regulation of dendritic spine development	40	6	0.64	9.31	+	8.34E-05	2.07E-02
positive regulation of dendrite development	69	7	1.11	6.3	+	2.03E-04	3.77E-02
positive regulation of neuron projection development	262	20	4.22	4.74	+	2.80E-08	6.25E-05
positive regulation of neuron differentiation	348	22	5.61	3.92	+	1.30E-07	2.26E-04
positive regulation of neurogenesis	438	22	7.06	3.12	+	4.87E-06	2.46E-03
positive regulation of cell development	507	26	8.17	3.18	+	4.54E-07	3.95E-04
positive regulation of nervous system development	501	23	8.07	2.85	+	1.20E-05	4.69E-03
positive regulation of cell projection organization	354	24	5.7	4.21	+	9.80E-09	2.55E-05
positive regulation of cellular component organization	1179	45	18.99	2.37	+	1.68E-07	2.39E-04
positive regulation of cell morphogenesis involved in differentiation	144	11	2.32	4.74	+	3.84E-05	1.18E-02
negative regulation of microtubule depolymerization	**26**	**5**	**0.42**	**11.94**	**+**	**1.18E-04**	**2.59E-02**
negative regulation of cellular component organization	666	30	10.73	2.8	+	7.99E-07	5.95E-04
negative regulation of microtubule polymerization or depolymerizat	38	6	0.61	9.8	+	6.46E-05	1.71E-02
negative regulation of organelle organization	356	17	5.74	2.96	+	1.05E-04	2.50E-02
regulation of cytoskeleton organization	526	23	8.47	2.71	+	2.50E-05	8.33E-03
regulation of microtubule polymerization or depolymerization	79	8	1.27	6.29	+	7.24E-05	1.89E-02
regulation of microtubule cytoskeleton organization	186	13	3	4.34	+	1.87E-05	7.12E-03
regulation of microtubule-based process	216	15	3.48	4.31	+	4.61E-06	2.40E-03
negative regulation of protein complex disassembly	69	7	1.11	6.3	+	2.03E-04	3.82E-02
regulation of protein complex disassembly	109	9	1.76	5.13	+	1.12E-04	2.54E-02
regulation of microtubule depolymerization	30	6	0.48	12.41	+	1.98E-05	7.38E-03
cerebral cortex radially oriented cell migration	**30**	**5**	**0.48**	**10.35**	**+**	**2.14E-04**	**3.89E-02**
movement of cell or subcellular component	1510	44	24.33	1.81	+	1.87E-04	3.57E-02
regulation of microtubule polymerization	**48**	**7**	**0.77**	**9.05**	**+**	**2.50E-05**	**8.50E-03**
regulation of protein polymerization	223	13	3.59	3.62	+	1.08E-04	2.53E-02
axonal transport	**48**	**6**	**0.77**	**7.76**	**+**	**2.07E-04**	**3.80E-02**
transport along microtubule	140	10	2.26	4.43	+	1.45E-04	2.98E-02
microtubule-based transport	140	10	2.26	4.43	+	1.45E-04	3.02E-02

GO BP complete	N REF (21,042)	N Set (339)	expected	Fold Enrichment	over(+) or under(-) represenatio	raw P	FDR
microtubule-based process	698	29	11.25	2.58	+	5.60E-06	2.50E-03
cytoskeleton-dependent intracellular transport	161	12	2.59	4.63	+	2.16E-05	7.67E-03
establishment of localization in cell	1779	49	28.66	1.71	+	2.63E-04	4.20E-02
vesicle cytoskeletal trafficking	**50**	**6**	**0.81**	**7.45**	**+**	**2.53E-04**	**4.17E-02**
organelle transport along microtubule	**71**	**7**	**1.14**	**6.12**	**+**	**2.38E-04**	**4.10E-02**
dendrite development	**99**	**9**	**1.59**	**5.64**	**+**	**5.62E-05**	**1.54E-02**
neuron projection development	653	26	10.52	2.47	+	5.08E-05	1.45E-02
plasma membrane bounded cell projection organization	1097	40	17.67	2.26	+	2.22E-06	1.58E-03
cell projection organization	1134	41	18.27	2.24	+	2.77E-06	1.67E-03
neuron development	798	32	12.86	2.49	+	4.99E-06	2.44E-03
neuron differentiation	988	35	15.92	2.2	+	2.58E-05	8.24E-03
neuron migration	**118**	**10**	**1.9**	**5.26**	**+**	**3.82E-05**	**1.19E-02**
regulation of axon extension	**96**	**8**	**1.55**	**5.17**	**+**	**2.53E-04**	**4.21E-02**
negative regulation of neuron projection development	**148**	**12**	**2.38**	**5.03**	**+**	**9.83E-06**	**4.15E-03**
negative regulation of neuron differentiation	220	13	3.54	3.67	+	9.53E-05	2.33E-02
negative regulation of neurogenesis	274	14	4.41	3.17	+	2.21E-04	3.97E-02
negative regulation of cell projection organization	175	13	2.82	4.61	+	1.02E-05	4.19E-03
protein-containing complex localization	**246**	**13**	**3.96**	**3.28**	**+**	**2.70E-04**	**4.27E-02**
axonogenesis	**358**	**17**	**5.77**	**2.95**	**+**	**1.13E-04**	**2.51E-02**
axon development	389	18	6.27	2.87	+	9.72E-05	2.34E-02
cell part morphogenesis	500	20	8.06	2.48	+	2.63E-04	4.24E-02
cell morphogenesis involved in neuron differentiation	419	19	6.75	2.81	+	8.06E-05	2.03E-02
microtubule cytoskeleton organization	**486**	**22**	**7.83**	**2.81**	**+**	**2.28E-05**	**7.93E-03**
cytoskeleton organization	1111	36	17.9	2.01	+	1.25E-04	2.64E-02
organelle organization	3387	89	54.57	1.63	+	2.42E-06	1.65E-03
endomembrane system organization	**380**	**17**	**6.12**	**2.78**	**+**	**2.21E-04**	**3.93E-02**
chemical synaptic transmission	**456**	**19**	**7.35**	**2.59**	**+**	**2.29E-04**	**4.02E-02**
anterograde trans-synaptic signaling	456	19	7.35	2.59	+	2.29E-04	3.98E-02
trans-synaptic signaling	464	19	7.48	2.54	+	2.82E-04	4.33E-02
synaptic signaling	465	19	7.49	2.54	+	2.90E-04	4.40E-02
cell projection assembly	**460**	**19**	**7.41**	**2.56**	**+**	**2.54E-04**	**4.14E-02**
cellular component assembly	2504	67	40.34	1.66	+	4.56E-05	1.34E-02

GO BP complete	N REF (21,042)	N Set (339)	expected	Fold Enrichment	over(+) or under(-) represenatio	raw P	FDR
cellular component biogenesis	2728	71	43.95	1.62	+	6.08E-05	1.64E-02
regulation of cellular localization	**802**	**32**	**12.92**	**2.48**	**+**	**5.29E-06**	**2.51E-03**
regulation of localization	2607	69	42	1.64	+	4.33E-05	1.30E-02
ubiquitin-dependent protein catabolic process	**502**	**20**	**8.09**	**2.47**	**+**	**2.76E-04**	**4.32E-02**
modification-dependent protein catabolic process	526	23	8.47	2.71	+	2.50E-05	8.16E-03
proteolysis involved in cellular protein catabolic process	584	23	9.41	2.44	+	1.68E-04	3.28E-02
cellular protein catabolic process	613	24	9.88	2.43	+	1.22E-04	2.60E-02
cellular protein metabolic process	3700	90	59.61	1.51	+	5.34E-05	1.49E-02
cellular macromolecule metabolic process	6569	138	105.83	1.3	+	2.47E-04	4.16E-02
modification-dependent macromolecule catabolic process	536	24	8.64	2.78	+	1.15E-05	4.61E-03
protein ubiquitination	**654**	**24**	**10.54**	**2.28**	**+**	**2.44E-04**	**4.14E-02**
cellular protein modification process	3065	82	49.38	1.66	+	4.16E-06	2.33E-03
protein modification process	3065	82	49.38	1.66	+	4.16E-06	2.25E-03
macromolecule modification	3281	87	52.86	1.65	+	2.56E-06	1.67E-03
regulation of transport	**1788**	**52**	**28.81**	**1.81**	**+**	**5.07E-05**	**1.47E-02**
phosphate-containing compound metabolic process	**2069**	**56**	**33.33**	**1.68**	**+**	**1.53E-04**	**3.07E-02**
phosphorus metabolic process	2165	58	34.88	1.66	+	1.45E-04	2.95E-02
immune response	**1825**	**12**	**29.4**	**0.41**	**-**	**2.78E-04**	**4.31E-02**
detection of stimulus involved in sensory perception	**531**	**0**	**8.55**	**< 0.01**	**-**	**3.12E-04**	**4.64E-02**

Table E9. Over- or under-represented Gene Ontology biological process terms for the genes positively coexpressed with *DAAM1* exclusively in the primary visual cort

The gene list analysis was carried out using the analysis tool in the PANTHER classification system (PMID: 23868073), with GO annotation data (PMID: 27899567). The GO terms were organized *hierarchially*, where the most post specific terms, indicated by bolded texts, were listed before the more general terms. The background gene set contains all 21,042 genes available in PANTHER 13.1 version. The test set contains the 409 protein-coding genes whose expression levels were positively correlated with *DAAM1* expression levels in the primary visual cortex area (V1C), but not in the other cortical regions in the prenatal brains. We used r ≥0.56 as the cut-off for positive-correlation coefficient, which was taken to be the 99th percentile of the empirical distribution of the correlation coefficients between *DAAM1* expression levels and the expression levels of all the other 60,153 coding and non-coding genes in neo-cortical regions of prenatal brains available in the BrainSpan database (http://www.brainspan.org/). The Pearson correlation coefficients were obtained using the vector of mRNA expression levels of each gene across all prenatal stages. For the regions that were not well parcellated during 8 – 10 post-conception weeks, their data were either merged (M1C and S1C) or used to represent the expression

GO BP complete	N REF (21,042)	N Set (409)	expected	Fold Enrichment	over(+) or under(-) represenatio	raw P	FDR
cristae formation	**31**	**9**	**0.87**	**10.37**	**+**	**9.96E-07**	**6.18E-04**
inner mitochondrial membrane organization	41	9	1.15	7.84	+	7.16E-06	2.58E-03
mitochondrial membrane organization	129	16	3.61	4.43	+	2.25E-06	1.09E-03
mitochondrion organization	437	39	12.23	3.19	+	1.11E-09	1.72E-05
organelle organization	3182	128	89.07	1.44	+	2.73E-05	6.95E-03
cellular component organization	5273	196	147.6	1.33	+	1.15E-05	3.79E-03
cellular process	15084	467	422.23	1.11	+	3.43E-05	8.05E-03
cellular component organization or biogenesis	5498	207	153.9	1.35	+	1.98E-06	1.02E-03
membrane organization	836	46	23.4	1.97	+	2.88E-05	7.21E-03
mitochondrial ATP synthesis coupled proton transport	**21**	**6**	**0.59**	**10.21**	**+**	**7.22E-05**	**1.51E-02**
mitochondrial transport	243	20	6.8	2.94	+	3.83E-05	8.61E-03
transport	4324	159	121.04	1.31	+	2.44E-04	4.02E-02
ATP synthesis coupled proton transport	29	8	0.81	9.86	+	5.54E-06	2.15E-03
ATP biosynthetic process	41	9	1.15	7.84	+	7.16E-06	2.64E-03
purine ribonucleotide biosynthetic process	121	13	3.39	3.84	+	7.73E-05	1.58E-02
ribonucleotide biosynthetic process	134	15	3.75	4	+	1.43E-05	4.42E-03
nucleotide biosynthetic process	203	18	5.68	3.17	+	3.79E-05	8.64E-03
nucleoside phosphate biosynthetic process	205	18	5.74	3.14	+	4.27E-05	9.32E-03
nucleoside phosphate metabolic process	525	39	14.7	2.65	+	1.14E-07	1.26E-04
organophosphate metabolic process	990	52	27.71	1.88	+	3.31E-05	7.90E-03
phosphorus metabolic process	2199	100	61.55	1.62	+	2.45E-06	1.12E-03
cellular metabolic process	9069	306	253.86	1.21	+	2.39E-05	6.39E-03
metabolic process	9969	330	279.05	1.18	+	4.00E-05	8.86E-03

GO BP complete	N REF (21,042)	N Set (409)	expected	Fold Enrichment	over(+) or under(-) represenatio	raw P	FDR
phosphate-containing compound metabolic process	2107	99	58.98	1.68	+	5.53E-07	3.73E-04
nucleobase-containing small molecule metabolic process	609	42	17.05	2.46	+	2.58E-07	2.35E-04
primary metabolic process	9162	303	256.46	1.18	+	1.48E-04	2.64E-02
nucleotide metabolic process	519	39	14.53	2.68	+	8.63E-08	1.03E-04
ribose phosphate biosynthetic process	138	15	3.86	3.88	+	1.96E-05	5.52E-03
carbohydrate derivative metabolic process	1094	54	30.62	1.76	+	1.13E-04	2.17E-02
ribose phosphate metabolic process	397	32	11.11	2.88	+	3.04E-07	2.48E-04
ribonucleotide metabolic process	381	31	10.66	2.91	+	3.86E-07	2.99E-04
purine nucleotide biosynthetic process	128	14	3.58	3.91	+	3.46E-05	8.01E-03
purine-containing compound biosynthetic process	141	14	3.95	3.55	+	9.05E-05	1.80E-02
organonitrogen compound biosynthetic process	1438	69	40.25	1.71	+	2.41E-05	6.33E-03
organonitrogen compound metabolic process	5534	222	154.91	1.43	+	2.81E-09	1.45E-05
purine-containing compound metabolic process	422	30	11.81	2.54	+	1.09E-05	3.67E-03
purine nucleotide metabolic process	385	30	10.78	2.78	+	1.37E-06	7.56E-04
purine ribonucleotide metabolic process	366	29	10.24	2.83	+	1.50E-06	8.03E-04
purine ribonucleoside triphosphate biosynthetic process	53	11	1.48	7.41	+	1.12E-06	6.66E-04
purine ribonucleoside triphosphate metabolic process	235	27	6.58	4.1	+	3.55E-09	1.38E-05
ribonucleoside triphosphate metabolic process	241	28	6.75	4.15	+	1.45E-09	1.12E-05
nucleoside triphosphate metabolic process	262	28	7.33	3.82	+	7.78E-09	1.51E-05
purine nucleoside triphosphate metabolic process	242	27	6.77	3.99	+	6.29E-09	1.39E-05
purine nucleoside triphosphate biosynthetic process	54	11	1.51	7.28	+	1.31E-06	7.54E-04
nucleoside triphosphate biosynthetic process	70	12	1.96	6.12	+	2.17E-06	1.08E-03
ribonucleoside triphosphate biosynthetic process	59	12	1.65	7.27	+	4.40E-07	3.25E-04
ATP metabolic process	204	25	5.71	4.38	+	4.17E-09	1.29E-05
purine ribonucleoside monophosphate metabolic process	246	26	6.89	3.78	+	3.28E-08	5.08E-05
purine nucleoside monophosphate metabolic process	247	26	6.91	3.76	+	3.53E-08	4.98E-05
nucleoside monophosphate metabolic process	274	28	7.67	3.65	+	1.89E-08	3.25E-05
ribonucleoside monophosphate metabolic process	259	28	7.25	3.86	+	6.19E-09	1.60E-05
drug metabolic process	615	36	17.21	2.09	+	6.68E-05	1.42E-02
purine ribonucleoside monophosphate biosynthetic process	64	10	1.79	5.58	+	3.11E-05	7.66E-03
purine nucleoside monophosphate biosynthetic process	64	10	1.79	5.58	+	3.11E-05	7.54E-03
nucleoside monophosphate biosynthetic process	87	12	2.44	4.93	+	1.59E-05	4.83E-03

GO BP complete	N REF (21,042)	N Set (409)	expected	Fold Enrichment	over(+) or under(-) represenatio	raw P	FDR
ribonucleoside monophosphate biosynthetic process	77	12	2.16	5.57	+	5.22E-06	2.08E-03
energy coupled proton transport, down electrochemical gradient	29	8	0.81	9.86	+	5.54E-06	2.10E-03
hydrogen ion transmembrane transport	119	15	3.33	4.5	+	3.88E-06	1.58E-03
transmembrane transport	1225	64	34.29	1.87	+	3.41E-06	1.43E-03
proton transport	151	16	4.23	3.79	+	1.40E-05	4.42E-03
monovalent inorganic cation transport	420	26	11.76	2.21	+	3.03E-04	4.66E-02
protein peptidyl-prolyl isomerization	**44**	**9**	**1.23**	**7.31**	**+**	**1.18E-05**	**3.81E-03**
peptidyl-proline modification	59	9	1.65	5.45	+	9.12E-05	1.79E-02
cellular protein modification process	3164	123	88.57	1.39	+	1.87E-04	3.25E-02
protein modification process	3164	123	88.57	1.39	+	1.87E-04	3.22E-02
protein metabolic process	4466	174	125.01	1.39	+	3.32E-06	1.43E-03
macromolecule modification	3451	131	96.6	1.36	+	3.09E-04	4.65E-02
cellular protein metabolic process	3752	156	105.02	1.49	+	2.89E-07	2.49E-04
response to amine	**40**	**7**	**1.12**	**6.25**	**+**	**2.62E-04**	**4.27E-02**
mitochondrial electron transport, NADH to ubiquinone	**49**	**8**	**1.37**	**5.83**	**+**	**1.47E-04**	**2.65E-02**
respiratory electron transport chain	112	17	3.14	5.42	+	8.30E-08	1.07E-04
cellular respiration	167	19	4.67	4.06	+	8.48E-07	5.48E-04
energy derivation by oxidation of organic compounds	240	21	6.72	3.13	+	1.06E-05	3.64E-03
generation of precursor metabolites and energy	376	27	10.52	2.57	+	1.82E-05	5.32E-03
electron transport chain	182	19	5.09	3.73	+	2.73E-06	1.21E-03
mitochondrial ATP synthesis coupled electron transport	91	15	2.55	5.89	+	1.85E-07	1.92E-04
ATP synthesis coupled electron transport	92	15	2.58	5.82	+	2.10E-07	2.04E-04
oxidative phosphorylation	100	15	2.8	5.36	+	5.47E-07	3.86E-04
phosphorylation	1289	64	36.08	1.77	+	1.94E-05	5.57E-03
SCF-dependent proteasomal ubiquitin-dependent protein catabolic	**73**	**11**	**2.04**	**5.38**	**+**	**1.71E-05**	**5.09E-03**
proteasome-mediated ubiquitin-dependent protein catabolic process	294	23	8.23	2.79	+	2.18E-05	5.93E-03
proteasomal protein catabolic process	319	24	8.93	2.69	+	2.63E-05	6.78E-03
cellular protein catabolic process	579	33	16.21	2.04	+	2.07E-04	3.52E-02
ubiquitin-dependent protein catabolic process	492	29	13.77	2.11	+	3.04E-04	4.63E-02
modification-dependent protein catabolic process	497	30	13.91	2.16	+	1.82E-04	3.21E-02
modification-dependent macromolecule catabolic process	506	31	14.16	2.19	+	1.19E-04	2.25E-02
mitochondrial respiratory chain complex assembly	**96**	**13**	**2.69**	**4.84**	**+**	**8.48E-06**	**2.99E-03**

GO BP complete	N REF (21,042)	N Set (409)	expected	Fold Enrichment	over(+) or under(-) represenatio	raw P	FDR
cellular protein complex assembly	418	31	11.7	2.65	+	2.39E-06	1.12E-03
protein complex subunit organization	1321	61	36.98	1.65	+	2.14E-04	3.61E-02
positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	**77**	**10**	**2.16**	**4.64**	**+**	**1.26E-04**	**2.33E-02**
positive regulation of ubiquitin protein ligase activity	85	10	2.38	4.2	+	2.63E-04	4.25E-02
regulation of ubiquitin-protein transferase activity	125	13	3.5	3.72	+	1.04E-04	2.03E-02
positive regulation of ubiquitin-protein transferase activity	104	12	2.91	4.12	+	7.78E-05	1.57E-02
NIK/NF-kappaB signaling	**86**	**10**	**2.41**	**4.15**	**+**	**2.87E-04**	**4.53E-02**
negative regulation of ubiquitin-protein transferase activity	**86**	**10**	**2.41**	**4.15**	**+**	**2.87E-04**	**4.49E-02**
mitochondrial translational elongation	**86**	**10**	**2.41**	**4.15**	**+**	**2.87E-04**	**4.44E-02**
translational elongation	121	12	3.39	3.54	+	2.86E-04	4.57E-02
Wnt signaling pathway, planar cell polarity pathway	**101**	**11**	**2.83**	**3.89**	**+**	**2.43E-04**	**4.05E-02**
post-translational protein modification	**440**	**28**	**12.32**	**2.27**	**+**	**1.25E-04**	**2.33E-02**
detection of chemical stimulus involved in sensory perception of smell	**429**	**1**	**12.01**	**0.08**	**-**	**1.38E-04**	**2.52E-02**
detection of chemical stimulus involved in sensory perception	472	1	13.21	0.08	-	4.49E-05	9.67E-03
sensory perception of chemical stimulus	533	2	14.92	0.13	-	7.33E-05	1.52E-02
detection of chemical stimulus	507	1	14.19	0.07	-	2.17E-05	6.00E-03

Table E10. Genome Wide Association Study (GWAS) Sources for Genetic Correlations with PC1-SA and PC2-SA

Phenotype	Sample size	Reference	Download link	Ancestry
Cognitive Function	269,867	Savage, J. E. et al. Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. *Nat Genet* 50, 912–919 (2018).	https://ctg.cncr.nl/software/summary_statistics	European
Educational Attainment	766,345	Lee, J. J. et al. Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nat Genet 50, 1112–1121 (2018).	https://www.thessgac.org/data	European
Height	693,529	Yengo, L. et al. Meta-analysis of genome-wide association studies for height and body mass index in ~700000 individuals of European ancestry. Hum Mol Genet 27, 3641–3649 (2018).	http://portals.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium_data_file	European
Birth Weight	298,142	Warrington, N. M. et al. Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nat Genet 51, 804–814	www.egg-consortium.org	European
Alzheimer's Disease	21,982 cases; 41,944 controls (stage 1 largest available)	Kunkle, B. W. et al. Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates Aβ, tau, immunity and lipid processing. Nat Genet 51, 414–430 (2019).	https://www.niagads.org/datasets/ng00075	European
Schizophrenia	33,640 cases; 43,456 controls	Schizophrenia Working Group of the Psychiatric Genomics Consortium et al. Biological insights from 108 schizophrenia-associated genetic loci. Nature 511, 421–427 (2014).	https://www.med.unc.edu/pgc/results-and-downloads/	European
Major Depressive Disorder	170,756 cases; 329,443 controls	Wray, N. R. et al. Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nat Genet 50, 668–681 (2018).	https://www.med.unc.edu/pgc/results-and-downloads/	European
Attention Deficit Hyperactivity Disorder	19,099 cases; 34,194 controls	Demontis, D. et al. Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nat Genet 51, 63–75 (2019).	https://www.med.unc.edu/pgc/results-and-downloads/	European
Bipolar Disorder	20,352 cases; 31,358 controls	Stahl, E. A. et al. Genome-wide association study identifies 30 loci associated with bipolar disorder. Nat Genet 51, 793–803 (2019).	https://www.med.unc.edu/pgc/results-and-downloads/	European

Table E11. Genetic Correlation Results Between PC1.SA and PC2.SA and Complex Traits Using LD Score Regression (LDSC)

Genetic correlations were conducted between PC1.SA and PC2.SA and complex traits (related to growth, brain function, and brain disorders) using LD Score Regression (LDSC) v1.0.0 (https://github.com/bulik/ldsc/wiki/Heritability-and-Genetic-Correlation). Single nucleotide polymorphisms (SNPs) were filtered using the available HapMap3 SNPs and genetic correlations were conducted using LDSC's 1000 Genomes European LD scores. Genetic correlations were restricted to European GWAS samples (Table E9). A Bonferroni correction was applied to correct for the 55 genetic correlations. The required LDSC files were obtained from the LDSC GitHub repository (https://data.broadinstitute.org/alkesgroup/LDSCORE/).

phenotype1	phenotype2	r_g	se	z	pRAW	pFWE (55 tests)
PC1	PC2	-0.0597	0.0562	-1.0624	2.88E-01	1
PC1	Cognitive Function	0.1736	0.0347	5.0004	5.72E-07	3.15E-05
PC1	Educational Attainment	0.2095	0.0296	7.088	1.36E-12	7.48E-11
PC1	Height	0.2307	0.0317	7.2689	3.62E-13	1.99E-11
PC1	Birth Weight	0.2183	0.0376	5.8008	6.60E-09	3.63E-07
PC1	Alzheimer's Disease	-0.0688	0.0866	-0.7949	4.27E-01	1
PC1	Schizophrenia	0.0195	0.0407	0.4803	6.31E-01	1
PC1	MDD	-0.0556	0.0349	-1.5922	1.11E-01	1
PC1	ADHD	-0.0958	0.0481	-1.9894	4.67E-02	1
PC1	Bipolar Disorder	0.1151	0.046	2.5033	1.23E-02	6.77E-01
PC2	PC1	-0.0597	0.0562	-1.0624	2.88E-01	1
PC2	Cognitive Function	-0.082	0.0309	-2.6531	7.98E-03	4.39E-01
PC2	Educational Attainment	-0.0419	0.0284	-1.4747	1.40E-01	1
PC2	Height	-0.0741	0.0252	-2.9402	3.28E-03	1.80E-01
PC2	Birth Weight	-0.0724	0.0341	-2.1223	3.38E-02	1
PC2	Alzheimer's Disease	0.0252	0.0825	0.3056	7.60E-01	1
PC2	Schizophrenia	0.006	0.033	0.1805	8.57E-01	1
PC2	MDD	0.0158	0.0336	0.4696	6.39E-01	1
PC2	ADHD	0.0047	0.0481	0.098	9.22E-01	1
PC2	Bipolar Disorder	0.068	0.0458	1.4861	1.37E-01	1
Cognitive Function	PC1	0.1736	0.0347	5.0004	5.72E-07	3.15E-05
Cognitive Function	PC2	-0.082	0.0309	-2.6531	7.98E-03	4.39E-01
Cognitive Function	Educational Attainment	0.7274	0.0111	65.4938	0	0
Cognitive Function	Height	0.1155	0.0142	8.1376	4.03E-16	2.22E-14
Cognitive Function	Birth Weight	0.111	0.021	5.2844	1.26E-07	6.94E-06
Cognitive Function	Alzheimer's Disease	-0.3038	0.0781	-3.8881	1.01E-04	5.56E-03
Cognitive Function	Schizophrenia	-0.2017	0.0217	-9.3042	1.35E-20	7.43E-19

phenotype1	phenotype2	r_g	se	z	pRAW	pFWE (55 tests)
Cognitive Function	MDD	-0.101	0.0193	-5.2434	1.58E-07	8.67E-06
Cognitive Function	ADHD	-0.3683	0.0307	-12.0084	3.21E-33	1.77E-31
Cognitive Function	Bipolar Disorder	-0.0398	0.024	-1.6562	9.77E-02	1
Educational Attainment	PC1	0.2095	0.0296	7.088	1.36E-12	7.48E-11
Educational Attainment	PC2	-0.0419	0.0284	-1.4747	1.40E-01	1
Educational Attainment	Cognitive Function	0.7274	0.0111	65.4938	0.00E+00	0.00E+00
Educational Attainment	Height	0.138	0.0116	11.876	1.58E-32	8.68E-31
Educational Attainment	Birth Weight	0.1123	0.0186	6.0368	1.57E-09	8.65E-08
Educational Attainment	Alzheimer's Disease	-0.2149	0.054	-3.9776	6.96E-05	3.83E-03
Educational Attainment	Schizophrenia	0.0626	0.0196	3.1893	1.43E-03	7.87E-02
Educational Attainment	MDD	-0.1734	0.0185	-9.3725	7.09E-21	3.90E-19
Educational Attainment	ADHD	-0.5159	0.0255	-20.2651	2.61E-91	1.44E-89
Educational Attainment	Bipolar Disorder	0.182	0.021	8.6607	4.69E-18	2.58E-16
Height	PC1	0.2307	0.0317	7.2689	3.62E-13	1.99E-11
Height	PC2	-0.0741	0.0252	-2.9402	3.28E-03	1.80E-01
Height	Cognitive Function	0.1155	0.0142	8.1376	4.03E-16	2.22E-14
Height	Educational Attainment	0.138	0.0116	11.876	1.58E-32	8.68E-31
Height	Birth Weight	0.3618	0.0198	18.2287	3.05E-74	1.68E-72
Height	Alzheimer's Disease	-0.1324	0.0434	-3.0521	2.27E-03	1.25E-01
Height	Schizophrenia	-0.0103	0.0174	-0.5929	5.53E-01	1
Height	MDD	-0.0528	0.0143	-3.7025	2.14E-04	1.17E-02
Height	ADHD	-0.0644	0.023	-2.7976	5.15E-03	2.83E-01
Height	Bipolar disorder	-0.0152	0.0221	-0.6877	4.92E-01	1
Birth Weight	PC1	0.2183	0.0376	5.8008	6.60E-09	3.63E-07
Birth Weight	PC2	-0.0724	0.0341	-2.1223	3.38E-02	1
Birth Weight	Cognitive Function	0.111	0.021	5.2844	1.26E-07	6.94E-06
Birth Weight	Educational Attainment	0.1123	0.0186	6.0368	1.57E-09	8.65E-08
Birth Weight	Height	0.3618	0.0198	18.2287	3.05E-74	1.68E-72
Birth Weight	Alzheimer's Disease	0.0339	0.0536	0.6322	5.27E-01	1
Birth Weight	Schizophrenia	0.0045	0.0256	0.1764	8.60E-01	1
Birth Weight	MDD	-0.0126	0.0189	-0.6691	5.03E-01	1
Birth Weight	ADHD	-0.0977	0.0327	-2.9842	2.84E-03	1.56E-01
Birth Weight	Bipolar disorder	0.0134	0.0294	0.4538	6.50E-01	1
Alzheimer's Disease	PC1	-0.0688	0.0866	-0.7949	4.27E-01	1

phenotype1	phenotype2	r_g	se	z	pRAW	pFWE (55 tests)
Alzheimer's Disease	PC2	0.0252	0.0825	0.3056	7.60E-01	1
Alzheimer's Disease	Cognitive Function	-0.3038	0.0781	-3.8881	1.01E-04	5.56E-03
Alzheimer's Disease	Educational Attainment	-0.2149	0.054	-3.9776	6.96E-05	3.83E-03
Alzheimer's Disease	Height	-0.1324	0.0434	-3.0521	2.27E-03	1.25E-01
Alzheimer's Disease	Birth Weight	0.0339	0.0536	0.6322	5.27E-01	1
Alzheimer's Disease	Schizophrenia	0.07	0.0499	1.4016	1.61E-01	1
Alzheimer's Disease	MDD	-0.0172	0.0575	-0.2988	7.65E-01	1
Alzheimer's Disease	ADHD	0.0452	0.0921	0.4908	6.24E-01	1
Alzheimer's Disease	Bipolar Disorder	-0.0038	0.0618	-0.0616	9.51E-01	1
Schizophrenia	PC1	0.0195	0.0407	0.4803	6.31E-01	1
Schizophrenia	PC2	0.006	0.033	0.1805	8.57E-01	1
Schizophrenia	Cognitive Function	-0.2017	0.0217	-9.3042	1.35E-20	7.43E-19
Schizophrenia	Educational Attainment	0.0626	0.0196	3.1893	1.43E-03	7.87E-02
Schizophrenia	Height	-0.0103	0.0174	-0.5929	5.53E-01	1
Schizophrenia	Birth Weight	0.0045	0.0256	0.1764	8.60E-01	1
Schizophrenia	Alzheimer's Disease	0.07	0.0499	1.4016	1.61E-01	1
Schizophrenia	MDD	0.3137	0.0244	12.8737	6.33E-38	3.48E-36
Schizophrenia	ADHD	0.1243	0.0362	3.433	5.97E-04	3.28E-02
Schizophrenia	Bipolar Disorder	0.6816	0.0212	32.2246	8.00E-228	4.40E-226
MDD	PC1	-0.0556	0.0349	-1.5922	1.11E-01	1
MDD	PC2	0.0158	0.0336	0.4696	6.39E-01	1
MDD	Cognitive Function	-0.101	0.0193	-5.2434	1.58E-07	8.67E-06
MDD	Educational Attainment	-0.1734	0.0185	-9.3725	7.09E-21	3.90E-19
MDD	Height	-0.0528	0.0143	-3.7025	2.14E-04	1.17E-02
MDD	Birth Weight	-0.0126	0.0189	-0.6691	5.03E-01	1
MDD	Alzheimer's Disease	-0.0172	0.0575	-0.2988	7.65E-01	1
MDD	Schizophrenia	0.3137	0.0244	12.8737	6.33E-38	3.48E-36
MDD	ADHD	0.4537	0.0322	14.0913	4.30E-45	2.36E-43
MDD	Bipolar Disorder	0.332	0.0272	12.226	2.26E-34	1.24E-32
ADHD	PC1	-0.0958	0.0481	-1.9894	4.67E-02	1
ADHD	PC2	0.0047	0.0481	0.098	9.22E-01	1
ADHD	Cognitive Function	-0.3683	0.0307	-12.0084	3.21E-33	1.77E-31
ADHD	Educational Attainment	-0.5159	0.0255	-20.2651	2.61E-91	1.44E-89
ADHD	Height	-0.0644	0.023	-2.7976	5.15E-03	2.83E-01

phenotype1	phenotype2	r_g	se	z	pRAW	pFWE (55 tests)
ADHD	Birth Weight	-0.0977	0.0327	-2.9842	2.84E-03	1.56E-01
ADHD	Alzheimer's Disease	0.0452	0.0921	0.4908	6.24E-01	1
ADHD	Schizophrenia	0.1243	0.0362	3.433	5.97E-04	3.28E-02
ADHD	MDD	0.4537	0.0322	14.0913	4.30E-45	2.36E-43
ADHD	Bipolar Disorder	0.1205	0.0381	3.1621	1.57E-03	8.61E-02
Bipolar Disorder	PC1	0.1151	0.046	2.5033	1.23E-02	6.77E-01
Bipolar Disorder	PC2	0.068	0.0458	1.4861	1.37E-01	1
Bipolar Disorder	Cognitive Function	-0.0398	0.024	-1.6562	9.77E-02	1
Bipolar Disorder	Educational Attainment	0.182	0.021	8.6607	4.69E-18	2.58E-16
Bipolar Disorder	Height	-0.0152	0.0221	-0.6877	4.92E-01	1
Bipolar Disorder	Birth Weight	0.0134	0.0294	0.4538	6.50E-01	1
Bipolar Disorder	Alzheimer's Disease	-0.0038	0.0618	-0.0616	9.51E-01	1
Bipolar Disorder	Schizophrenia	0.6816	0.0212	32.2246	8.00E-228	4.40E-226
Bipolar Disorder	MDD	0.332	0.0272	12.226	2.26E-34	1.24E-32
Bipolar Disorder	ADHD	0.1205	0.0381	3.1621	1.57E-03	8.61E-02

Table E12A. Gene Co-Expression and Overrepresentation Test Results: PC1-SA (FDR-corrected) and PC2-SA comparison

First, genome-wide significant ($p \leq 5*10\text{-}8$) SNPs were mapped to genes using FUMA GWAS [1], resulting in 46 and 34 genes for PC1-SA and PC2-SA, respectively. Gene lists were filtered by the BrainSpan database of 52,376 genes, and one gene present in both lists was excluded, resulting in 44 and 31 genes for PC1-SA and PC2-SA, respectively. In order to identify gene co-expression networks, the top 0.1% positively correlated genes in BrainSpan [2] (filtered for prenatal and cortical samples) were retained for each "seed gene" in the PC1-SA and PC2-SA lists, seperately. Subsequently, the genes unique to PC1-SA and PC2-SA, respectively, were retained. Enrichment analyses for biological processes were conducted on each of the PC-SA lists using the PANTHER Overrepresentation Test (Released 20190711) and the GO Ontology database (Released 2019-07-03) [3]. An FDR correction was applied for multiple comparisons. The **FDR-corrected PC1-SA** results are indicated below, with corresponding PC2-SA p-values for these GO terms.

[1] K. Watanabe, E. Taskesen, A. van Bochoven and D. Posthuma. Functional mapping and annotation of genetic associations with FUMA. Nat. Commun. 8:1826. (2017).
[2] BrainSpan Atlas of the Developing Human Brain Miller, J.A. et al. (2014) Transcriptional landscape of the prenatal human brain, Nature 508: 199-206. doi:10.1038/nature13185
[3] PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. Huaiyu Mi, Anushya Muruganujan, Dustin Ebert, Xiaosong Huang and Paul D. Thomas Nucl. Acids Res. (2019) doi: 10.1093/nar/gky1038

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC1-SA.BS	expected	Fold Enrichment	direction	PC1.raw.p	PC1.FDR.p	PC2_p	PC2_fdr
protein-DNA complex disassembly	**21**	**8**	**1.38**	**5.78**	**+**	**0.000278**	**0.0233**	**1**	**1**
cellular component organization	5658	488	372.69	1.31	+	4.78E-11	2.37E-08	4.30E-13	1.37E-09
cellular process	14514	1078	956.03	1.13	+	1.37E-12	1.22E-09	2.72E-15	1.44E-11
cellular component organization or biogenesis	5850	515	385.34	1.34	+	3.19E-13	3.90E-10	1.25E-13	4.98E-10
protein-DNA complex subunit organization	242	33	15.94	2.07	+	0.000329	0.0265	0.00454	0.166
centrosome duplication	**29**	**9**	**1.91**	**4.71**	**+**	**0.000408**	**0.032**	**0.0859**	**0.876**
cell cycle process	979	119	64.49	1.85	+	1.59E-09	5.48E-07	3.51E-07	9.62E-05
cell cycle	1323	151	87.15	1.73	+	5.39E-10	2.09E-07	2.66E-11	5.29E-08
microtubule organizing center organization	92	18	6.06	2.97	+	0.000135	0.0132	0.001	0.0588
organelle organization	3410	331	224.62	1.47	+	1.25E-12	1.17E-09	1.42E-09	1.07E-06
chromosome separation	**31**	**9**	**2.04**	**4.41**	**+**	**0.000612**	**0.0442**	**0.251**	**1**
chromosome segregation	270	37	17.78	2.08	+	0.000104	0.0107	7.22E-08	2.94E-05
brain morphogenesis	**36**	**10**	**2.37**	**4.22**	**+**	**0.000414**	**0.032**	**0.721**	**1**
brain development	742	83	48.88	1.7	+	1.19E-05	0.00176	1.01E-05	0.0015
head development	786	85	51.77	1.64	+	2.82E-05	0.00371	1.18E-06	0.000279
anatomical structure development	5399	434	355.63	1.22	+	5.13E-06	0.00086	1.45E-10	1.92E-07
developmental process	5749	467	378.68	1.23	+	4.94E-07	0.000108	1.09E-10	1.58E-07

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC1-SA.BS	expected	Fold Enrichment	direction	PC1.raw.p	PC1.FDR.p	PC2_p	PC2_fdr
central nervous system development	982	98	64.68	1.52	+	0.000125	0.0124	3.21E-05	0.00365
nervous system development	2351	218	154.86	1.41	+	7.98E-07	0.000161	3.18E-08	1.49E-05
system development	4413	359	290.68	1.24	+	2.22E-05	0.00304	6.43E-11	1.02E-07
multicellular organism development	5012	405	330.14	1.23	+	8.75E-06	0.00134	2.09E-10	2.38E-07
anatomical structure morphogenesis	2145	186	141.29	1.32	+	0.000227	0.0203	2.86E-10	2.68E-07
somatic diversification of immune receptors	**47**	**13**	**3.1**	**4.2**	**+**	**6.11E-05**	**0.007**	**0.175**	**1**
synaptic vesicle endocytosis	**47**	**12**	**3.1**	**3.88**	**+**	**0.00022**	**0.0199**	**1**	**1**
synaptic vesicle recycling	55	13	3.62	3.59	+	0.000234	0.0207	1	1
establishment of localization in cell	1834	167	120.81	1.38	+	5.17E-05	0.00619	1.36E-05	0.00183
localization	5737	445	377.89	1.18	+	0.000117	0.0118	0.00029	0.0221
cellular localization	2453	227	161.58	1.4	+	5.22E-07	0.000112	1.58E-07	5.47E-05
vesicle-mediated transport in synapse	133	21	8.76	2.4	+	0.000584	0.0424	0.445	1
presynaptic endocytosis	47	12	3.1	3.88	+	0.00022	0.02	1	1
positive regulation of gene expression, epige	**64**	**15**	**4.22**	**3.56**	**+**	**8.64E-05**	**0.00928**	**0.173**	**1**
positive regulation of gene expression	1998	190	131.61	1.44	+	1.07E-06	0.000208	4.28E-06	0.000766
positive regulation of macromolecule metabolic p	3343	280	220.2	1.27	+	3.90E-05	0.00496	1.07E-05	0.00156
regulation of macromolecule metabolic process	6180	553	407.07	1.36	+	6.34E-16	1.68E-12	2.88E-06	0.000565
regulation of metabolic process	6707	591	441.79	1.34	+	4.87E-16	1.55E-12	1.70E-07	5.77E-05
regulation of biological process	11660	912	768.04	1.19	+	2.33E-14	3.71E-11	3.34E-11	5.91E-08
biological regulation	12352	969	813.62	1.19	+	5.63E-17	8.95E-13	1.70E-11	3.86E-08
positive regulation of metabolic process	3614	296	238.05	1.24	+	0.000105	0.0107	1.64E-05	0.00212
positive regulation of biological process	6166	486	406.15	1.2	+	7.83E-06	0.00122	1.04E-07	3.85E-05
regulation of gene expression	4495	428	296.08	1.45	+	1.47E-15	3.34E-12	5.05E-06	0.000874
regulation of gene expression, epigenetic	234	38	15.41	2.47	+	2.64E-06	0.000461	0.00421	0.16
histone lysine methylation	**72**	**15**	**4.74**	**3.16**	**+**	**0.000265**	**0.0226**	**0.295**	**1**
histone modification	363	61	23.91	2.55	+	6.56E-10	2.48E-07	0.02	0.413
covalent chromatin modification	374	63	24.64	2.56	+	3.13E-10	1.25E-07	0.0294	0.495
macromolecule metabolic process	6181	524	407.14	1.29	+	7.97E-11	3.62E-08	6.18E-10	5.46E-07
organic substance metabolic process	7853	619	517.27	1.2	+	6.12E-08	1.54E-05	1.17E-07	4.14E-05
metabolic process	8396	667	553.04	1.21	+	2.26E-09	7.19E-07	8.34E-08	3.16E-05

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC1-SA.BS	expected	Fold Enrichment	direction	PC1.raw.p	PC1.FDR.p	PC2_p	PC2_fdr
chromatin organization	695	97	45.78	2.12	+	8.83E-11	3.80E-08	0.00306	0.131
chromosome organization	1056	146	69.56	2.1	+	1.91E-15	3.79E-12	3.30E-08	1.50E-05
primary metabolic process	7495	595	493.69	1.21	+	6.24E-08	1.55E-05	1.06E-07	3.83E-05
nitrogen compound metabolic process	7006	570	461.48	1.24	+	4.15E-09	1.22E-06	1.26E-08	6.89E-06
cellular macromolecule metabolic process	5088	457	335.14	1.36	+	1.00E-12	9.96E-10	5.51E-08	2.31E-05
cellular metabolic process	7663	628	504.76	1.24	+	5.12E-11	2.40E-08	2.29E-10	2.28E-07
peptidyl-lysine modification	336	49	22.13	2.21	+	1.65E-06	0.000305	0.183	1
peptidyl-amino acid modification	898	93	59.15	1.57	+	6.25E-05	0.0071	0.000247	0.0198
DNA duplex unwinding	**109**	**21**	**7.18**	**2.92**	**+**	**4.71E-05**	**0.00586**	**0.00566**	**0.193**
DNA geometric change	118	21	7.77	2.7	+	0.000127	0.0125	0.00223	0.106
DNA conformation change	294	41	19.37	2.12	+	2.90E-05	0.00378	3.51E-06	0.000665
regulation of posttranscriptional gene silenc	**89**	**17**	**5.86**	**2.9**	**+**	**0.000263**	**0.0227**	**0.0183**	**0.394**
regulation of gene silencing	127	24	8.37	2.87	+	1.85E-05	0.00265	0.00669	0.218
regulation of cellular process	10941	868	720.68	1.2	+	1.12E-14	1.98E-11	1.02E-08	5.79E-06
regulation of gene silencing by RNA	**89**	**17**	**5.86**	**2.9**	**+**	**0.000263**	**0.0226**	**0.0183**	**0.393**
DNA-dependent DNA replication	**119**	**22**	**7.84**	**2.81**	**+**	**5.41E-05**	**0.00642**	**0.00908**	**0.27**
DNA replication	211	39	13.9	2.81	+	8.78E-08	2.12E-05	0.000524	0.0355
cellular macromolecule biosynthetic process	1716	181	113.03	1.6	+	2.44E-09	7.60E-07	0.035	0.534
macromolecule biosynthetic process	1768	181	116.46	1.55	+	1.73E-08	4.67E-06	0.0215	0.422
organic substance biosynthetic process	2862	256	188.52	1.36	+	9.55E-07	0.00019	0.0413	0.587
biosynthetic process	2938	263	193.53	1.36	+	6.73E-07	0.000141	0.0283	0.483
cellular biosynthetic process	2764	257	182.06	1.41	+	4.72E-08	1.21E-05	0.0529	0.671
neural tube closure	**93**	**17**	**6.13**	**2.78**	**+**	**0.000412**	**0.0319**	**0.108**	**0.856**
neural tube formation	108	19	7.11	2.67	+	0.000297	0.0246	0.136	0.99
morphogenesis of embryonic epithelium	147	25	9.68	2.58	+	7.48E-05	0.00843	0.15	0.937
tube morphogenesis	652	68	42.95	1.58	+	0.000502	0.0377	0.0287	0.489
tube closure	94	17	6.19	2.75	+	0.000459	0.0347	0.11	0.864
stem cell population maintenance	**139**	**25**	**9.16**	**2.73**	**+**	**2.59E-05**	**0.0035**	**0.0154**	**0.354**
maintenance of cell number	141	25	9.29	2.69	+	3.20E-05	0.00413	0.0166	0.373
histone acetylation	**117**	**21**	**7.71**	**2.72**	**+**	**0.000114**	**0.0116**	**0.684**	**1**

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC1-SA.BS	expected	Fold Enrichment	direction	PC1.raw.p	PC1.FDR.p	PC2_p	PC2_fdr
internal peptidyl-lysine acetylation	122	22	8.04	2.74	+	7.48E-05	0.00838	0.84	1
internal protein amino acid acetylation	127	23	8.37	2.75	+	4.89E-05	0.00594	0.845	1
protein acetylation	147	24	9.68	2.48	+	0.000159	0.0151	1	1
protein acylation	189	29	12.45	2.33	+	9.45E-05	0.00996	1	1
peptidyl-lysine acetylation	125	22	8.23	2.67	+	0.000102	0.0107	0.842	1
nuclear-transcribed mRNA catabolic process	**195**	**34**	**12.84**	**2.65**	**+**	**2.26E-06**	**0.000408**	**1**	**1**
mRNA catabolic process	213	35	14.03	2.49	+	6.38E-06	0.00106	0.647	1
negative regulation of gene expression	1716	173	113.03	1.53	+	1.06E-07	2.44E-05	0.000729	0.0466
negative regulation of macromolecule metabolic	2644	243	174.16	1.4	+	2.65E-07	5.85E-05	0.000144	0.0126
negative regulation of metabolic process	2890	264	190.36	1.39	+	1.28E-07	2.90E-05	3.42E-05	0.00381
negative regulation of biological process	5276	449	347.53	1.29	+	3.65E-09	1.09E-06	7.91E-08	3.07E-05
RNA catabolic process	244	38	16.07	2.36	+	7.80E-06	0.00124	0.202	1
RNA metabolic process	1677	175	110.46	1.58	+	1.03E-08	2.82E-06	0.0435	0.607
nucleic acid metabolic process	2277	257	149.99	1.71	+	2.16E-16	8.59E-13	0.00107	0.0616
nucleobase-containing compound metabolic proc	2788	282	183.64	1.54	+	1.69E-12	1.34E-09	0.00034	0.0249
organic cyclic compound metabolic process	3243	301	213.62	1.41	+	2.11E-09	6.86E-07	0.000253	0.0202
cellular nitrogen compound metabolic process	3425	324	225.6	1.44	+	5.09E-11	2.45E-08	0.000737	0.0467
heterocycle metabolic process	2968	291	195.5	1.49	+	1.82E-11	1.07E-08	0.00041	0.029
cellular aromatic compound metabolic process	3008	294	198.14	1.48	+	1.81E-11	1.11E-08	0.000268	0.021
nucleobase-containing compound catabolic proce	371	47	24.44	1.92	+	7.92E-05	0.00857	0.356	1
aromatic compound catabolic process	435	52	28.65	1.81	+	0.000122	0.0122	0.242	1
cellular nitrogen compound catabolic process	420	49	27.67	1.77	+	0.000306	0.025	0.448	1
organic cyclic compound catabolic process	469	57	30.89	1.85	+	4.58E-05	0.00574	0.354	1
heterocycle catabolic process	419	51	27.6	1.85	+	9.21E-05	0.00983	0.447	1
cellular macromolecule catabolic process	897	89	59.09	1.51	+	0.000319	0.0258	0.00703	0.226
mRNA metabolic process	688	79	45.32	1.74	+	8.14E-06	0.00126	0.0411	0.588
G1/S transition of mitotic cell cycle	**121**	**20**	**7.97**	**2.51**	**+**	**0.000548**	**0.0401**	**0.0101**	**0.287**
mitotic cell cycle phase transition	272	37	17.92	2.07	+	0.000113	0.0115	2.96E-07	8.57E-05
cell cycle phase transition	280	39	18.44	2.11	+	5.05E-05	0.00608	2.16E-07	7.01E-05
mitotic cell cycle process	600	84	39.52	2.13	+	2.10E-09	6.97E-07	2.26E-10	2.40E-07

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC1-SA.BS	expected	Fold Enrichment	direction	PC1.raw.p	PC1.FDR.p	PC2_p	PC2_fdr
mitotic cell cycle	687	98	45.25	2.17	+	2.40E-11	1.37E-08	1.55E-09	1.08E-06
cell cycle G1/S phase transition	122	20	8.04	2.49	+	0.000582	0.0425	0.00513	0.181
RNA export from nucleus	**129**	**21**	**8.5**	**2.47**	**+**	**0.00044**	**0.0336**	**0.0196**	**0.408**
RNA transport	197	29	12.98	2.23	+	0.00022	0.0202	0.0192	0.404
establishment of RNA localization	199	30	13.11	2.29	+	0.000137	0.0133	0.0284	0.483
RNA localization	220	32	14.49	2.21	+	0.000103	0.0108	0.0369	0.553
macromolecule localization	2489	222	163.95	1.35	+	7.63E-06	0.00123	0.000117	0.0104
nucleic acid transport	197	29	12.98	2.23	+	0.00022	0.0201	0.0192	0.403
nucleobase-containing compound transport	243	33	16.01	2.06	+	0.000338	0.027	0.0239	0.443
mRNA transport	**159**	**25**	**10.47**	**2.39**	**+**	**0.000276**	**0.0232**	**0.0813**	**0.849**
chromatin remodeling	**166**	**26**	**10.93**	**2.38**	**+**	**0.000201**	**0.0186**	**0.174**	**1**
mitotic nuclear division	**141**	**22**	**9.29**	**2.37**	**+**	**0.000488**	**0.0368**	**1.20E-06**	**0.000281**
regulation of Ras protein signal transduction	**244**	**38**	**16.07**	**2.36**	**+**	**7.80E-06**	**0.00123**	**0.194**	**1**
regulation of small GTPase mediated signal transc	346	48	22.79	2.11	+	6.79E-06	0.0011	1	1
regulation of intracellular signal transduction	1831	161	120.61	1.33	+	0.000363	0.0288	0.214	1
regulation of signal transduction	3128	257	206.04	1.25	+	0.000309	0.0251	0.0725	0.81
regulation of cell communication	3502	294	230.68	1.27	+	2.04E-05	0.00284	0.0373	0.556
regulation of signaling	3543	297	233.38	1.27	+	1.89E-05	0.00269	0.0464	0.617
protein export from nucleus	**150**	**23**	**9.88**	**2.33**	**+**	**0.000621**	**0.0447**	**0.0711**	**0.799**
cellular protein localization	1598	155	105.26	1.47	+	5.01E-06	0.000848	8.28E-06	0.00128
protein localization	2153	203	141.82	1.43	+	7.53E-07	0.000156	2.13E-05	0.00262
cellular macromolecule localization	1606	155	105.79	1.47	+	6.71E-06	0.0011	6.65E-06	0.00109
protein transport	1516	136	99.86	1.36	+	0.000543	0.04	0.00189	0.0929
establishment of protein localization	1609	143	105.98	1.35	+	0.000525	0.0392	0.000407	0.0289
peptide transport	1541	139	101.51	1.37	+	0.000402	0.0316	0.003	0.13
DNA recombination	**221**	**33**	**14.56**	**2.27**	**+**	**5.73E-05**	**0.0067**	**0.0373**	**0.556**
DNA metabolic process	745	101	49.07	2.06	+	2.04E-10	8.33E-08	0.000322	0.0239
double-strand break repair	**181**	**27**	**11.92**	**2.26**	**+**	**0.000236**	**0.0207**	**0.00891**	**0.266**
DNA repair	512	73	33.73	2.16	+	9.21E-09	2.62E-06	0.000137	0.012
cellular response to DNA damage stimulus	778	102	51.25	1.99	+	7.53E-10	2.79E-07	4.49E-05	0.00458

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC1-SA.BS	expected	Fold Enrichment	direction	PC1.raw.p	PC1.FDR.p	PC2_p	PC2_fdr
cellular response to stress	1704	165	112.24	1.47	+	2.22E-06	0.000407	1.16E-05	0.00164
regulation of G2/M transition of mitotic cell	**194**	**28**	**12.78**	**2.19**	**+**	**0.000347**	**0.0276**	**0.00442**	**0.164**
regulation of mitotic cell cycle phase transition	415	52	27.34	1.9	+	3.78E-05	0.00485	3.63E-05	0.00401
regulation of cell cycle phase transition	450	54	29.64	1.82	+	7.56E-05	0.0084	1.22E-05	0.00169
regulation of cell cycle process	761	93	50.13	1.86	+	9.15E-08	2.17E-05	3.98E-08	1.76E-05
regulation of cell cycle	1190	131	78.38	1.67	+	6.72E-08	1.64E-05	1.23E-09	9.76E-07
regulation of mitotic cell cycle	630	76	41.5	1.83	+	2.26E-06	0.000403	2.33E-08	1.16E-05
regulation of cell cycle G2/M phase transition	211	30	13.9	2.16	+	0.000234	0.0208	0.000263	0.0208
nuclear chromosome segregation	**215**	**31**	**14.16**	**2.19**	**+**	**0.000151**	**0.0145**	**1.12E-05**	**0.00161**
cell cycle checkpoint	**198**	**28**	**13.04**	**2.15**	**+**	**0.000422**	**0.0324**	**0.0121**	**0.321**
negative regulation of cell cycle	579	68	38.14	1.78	+	2.00E-05	0.00281	0.0207	0.417
negative regulation of cellular process	4701	401	309.65	1.29	+	3.70E-08	9.64E-06	2.65E-07	7.80E-05
protein-containing complex localization	**257**	**36**	**16.93**	**2.13**	**+**	**7.60E-05**	**0.0084**	**0.00244**	**0.113**
regulation of chromosome organization	**351**	**49**	**23.12**	**2.12**	**+**	**4.72E-06**	**0.000815**	**0.000158**	**0.0132**
regulation of organelle organization	1284	138	84.58	1.63	+	1.00E-07	2.35E-05	8.83E-05	0.00826
regulation of cellular component organization	2455	240	161.71	1.48	+	2.61E-09	8.00E-07	1.46E-06	0.000331
regulation of response to DNA damage stimu	**218**	**30**	**14.36**	**2.09**	**+**	**0.000449**	**0.0342**	**0.099**	**0.945**
negative regulation of cell cycle process	**331**	**44**	**21.8**	**2.02**	**+**	**4.83E-05**	**0.00596**	**0.000708**	**0.0456**
ribonucleoprotein complex biogenesis	**456**	**55**	**30.04**	**1.83**	**+**	**5.69E-05**	**0.0067**	**0.0968**	**0.929**
regulation of cellular protein localization	**543**	**61**	**35.77**	**1.71**	**+**	**0.00015**	**0.0145**	**0.00427**	**0.161**
regulation of cellular localization	917	93	60.4	1.54	+	0.000128	0.0125	0.00604	0.201
transcription by RNA polymerase II	**492**	**55**	**32.41**	**1.7**	**+**	**0.000409**	**0.0319**	**0.109**	**0.863**
transcription, DNA-templated	650	79	42.82	1.85	+	1.02E-06	2.00E-04	0.253	1
nucleic acid-templated transcription	651	79	42.88	1.84	+	1.46E-06	0.000272	0.189	1
RNA biosynthetic process	662	79	43.61	1.81	+	2.58E-06	0.000457	0.223	1
nucleobase-containing compound biosynthetic pr	1098	113	72.32	1.56	+	1.19E-05	0.00177	0.0245	0.452
organic cyclic compound biosynthetic process	1315	123	86.62	1.42	+	0.000224	0.0201	0.0282	0.482
heterocycle biosynthetic process	1169	115	77	1.49	+	5.91E-05	0.00681	0.04	0.577
cellular nitrogen compound biosynthetic process	1643	162	108.22	1.5	+	1.15E-06	0.000221	0.156	0.97
aromatic compound biosynthetic process	1177	116	77.53	1.5	+	4.85E-05	0.00594	0.0408	0.586

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC1-SA.BS	expected	Fold Enrichment	direction	PC1.raw.p	PC1.FDR.p	PC2_p	PC2_fdr
gene expression	2011	199	132.46	1.5	+	3.52E-08	9.34E-06	0.00456	0.166
organelle localization	**578**	**64**	**38.07**	**1.68**	**+**	**0.000164**	**0.0155**	**0.000222**	**0.018**
cell morphogenesis	**721**	**75**	**47.49**	**1.58**	**+**	**0.000296**	**0.0247**	**4.72E-05**	**0.00478**
plasma membrane bounded cell projection c	**1105**	**114**	**72.79**	**1.57**	**+**	**9.52E-06**	**0.00144**	**1.99E-05**	**0.00249**
cell projection organization	1148	117	75.62	1.55	+	1.05E-05	0.00157	2.38E-06	0.00052
regulation of cellular component biogenesis	**932**	**93**	**61.39**	**1.51**	**+**	**0.000189**	**0.0176**	**0.14**	**1**
negative regulation of cellular macromolecu	**1390**	**135**	**91.56**	**1.47**	**+**	**2.06E-05**	**0.00285**	**0.000407**	**0.029**
negative regulation of cellular biosynthetic proces	1525	145	100.45	1.44	+	2.81E-05	0.00373	0.000364	0.0265
negative regulation of cellular metabolic process	2546	224	167.7	1.34	+	1.66E-05	0.00242	8.06E-06	0.00127
regulation of cellular metabolic process	6245	541	411.36	1.32	+	7.00E-13	7.42E-10	1.59E-06	0.000355
regulation of cellular biosynthetic process	4216	390	277.71	1.4	+	3.35E-12	2.54E-09	4.84E-05	0.00488
regulation of biosynthetic process	4296	392	282.98	1.39	+	1.56E-11	9.93E-09	1.02E-05	0.00151
negative regulation of biosynthetic process	1550	146	102.1	1.43	+	4.04E-05	0.0051	0.000323	0.0238
regulation of cellular macromolecule biosynthetic	3952	375	260.32	1.44	+	3.60E-13	4.09E-10	3.14E-05	0.00359
regulation of macromolecule biosynthetic proces	4082	382	268.88	1.42	+	1.44E-12	1.20E-09	3.91E-05	0.00423
negative regulation of macromolecule biosynthet	1471	141	96.89	1.46	+	2.63E-05	0.00351	0.000456	0.0317
positive regulation of cellular component or	**1206**	**117**	**79.44**	**1.47**	**+**	**7.65E-05**	**0.00839**	**0.00027**	**0.0208**
positive regulation of cellular process	5409	445	356.29	1.25	+	2.53E-07	5.67E-05	3.08E-07	8.75E-05
regulation of nervous system development	**932**	**90**	**61.39**	**1.47**	**+**	**0.000669**	**0.0479**	**2.11E-05**	**0.00262**
regulation of transcription by RNA polymera	**2699**	**257**	**177.78**	**1.45**	**+**	**6.51E-09**	**1.88E-06**	**2.98E-05**	**0.00344**
regulation of transcription, DNA-templated	3516	330	231.6	1.42	+	7.98E-11	3.52E-08	0.00011	0.00986
regulation of nucleic acid-templated transcription	3574	336	235.42	1.43	+	3.95E-11	2.09E-08	8.77E-05	0.00825
regulation of RNA biosynthetic process	3579	336	235.75	1.43	+	4.09E-11	2.10E-08	7.43E-05	0.00721
regulation of RNA metabolic process	3826	366	252.02	1.45	+	3.09E-13	4.10E-10	1.47E-05	0.00195
regulation of nucleobase-containing compound m	4080	387	268.75	1.44	+	1.41E-13	2.04E-10	8.23E-06	0.00128
regulation of primary metabolic process	6051	522	398.58	1.31	+	4.98E-12	3.44E-09	8.99E-06	0.00136
regulation of nitrogen compound metabolic proce	5868	510	386.52	1.32	+	3.92E-12	2.83E-09	1.89E-05	0.00239
positive regulation of transcription, DNA-ter	**1547**	**144**	**101.9**	**1.41**	**+**	**7.77E-05**	**0.00846**	**3.61E-06**	**0.000675**
positive regulation of nucleic acid-templated tran	1634	147	107.63	1.37	+	0.000263	0.0225	2.20E-05	0.00265
positive regulation of RNA biosynthetic process	1635	147	107.7	1.36	+	0.000265	0.0224	1.34E-05	0.00184

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC1-SA.BS	expected	Fold Enrichment	direction	PC1.raw.p	PC1.FDR.p	PC2_p	PC2_fdr
positive regulation of RNA metabolic process	1719	158	113.23	1.4	+	5.87E-05	0.00682	2.67E-06	0.00056
positive regulation of nucleobase-containing com	1881	169	123.9	1.36	+	9.33E-05	0.00989	3.86E-06	0.000706
negative regulation of nucleobase-containin	**1433**	**133**	**94.39**	**1.41**	**+**	**0.000166**	**0.0155**	**0.00116**	**0.0649**
negative regulation of nitrogen compound metab	2346	198	154.53	1.28	+	0.00054	0.04	1.46E-05	0.00195
regulation of biological quality	**4041**	**325**	**266.18**	**1.22**	**+**	**0.000153**	**0.0145**	**0.0277**	**0.482**
G protein-coupled receptor signaling pathwa	**1302**	**54**	**85.76**	**0.63**	**-**	**3.00E-04**	**0.0246**	**1.72E-08**	**8.82E-06**
defense response	**1331**	**45**	**87.67**	**0.51**	**-**	**7.84E-07**	**0.00016**	**0.00797**	**0.247**
Unclassified	**3181**	**104**	**209.53**	**0.5**	**-**	**5.73E-17**	**3.04E-13**	**1.41E-15**	**1.12E-11**
humoral immune response mediated by circ	**167**	**1**	**11**	**0.09**	**-**	**0.000538**	**0.04**	**0.0131**	**0.326**
adaptive immune response	602	12	39.65	0.3	-	6.42E-07	0.000136	1.86E-07	6.16E-05
immune response	1848	75	121.73	0.62	-	4.92E-06	0.000842	0.00783	0.243
humoral immune response	344	5	22.66	0.22	-	2.54E-05	0.00345	0.0102	0.288
complement activation	**178**	**1**	**11.72**	**0.09**	**-**	**0.000248**	**0.0216**	**0.0271**	**0.475**
detection of chemical stimulus involved in se	**430**	**2**	**28.32**	**0.07**	**-**	**8.59E-10**	**3.10E-07**	**4.42E-07**	**0.000119**
detection of chemical stimulus involved in sensor	480	2	31.62	0.06	-	3.90E-11	2.14E-08	4.98E-08	2.14E-05
sensory perception of chemical stimulus	532	5	35.04	0.14	-	9.55E-10	3.37E-07	2.60E-08	1.25E-05
sensory perception	960	28	63.23	0.44	-	1.34E-06	0.000254	0.00244	0.113
system process	1958	90	128.97	0.7	-	0.000297	0.0245	0.155	0.966
detection of chemical stimulus	517	5	34.05	0.15	-	1.95E-09	6.61E-07	3.14E-07	8.77E-05
detection of stimulus	691	12	45.52	0.26	-	1.02E-08	2.85E-06	0.000915	0.0551
detection of stimulus involved in sensory percept	538	3	35.44	0.08	-	1.17E-11	7.72E-09	2.69E-06	0.000556
sensory perception of smell	460	2	30.3	0.07	-	1.21E-10	5.07E-08	9.83E-07	0.000244
keratinization	**225**	**1**	**14.82**	**0.07**	**-**	**1.82E-05**	**0.00263**	**0.048**	**0.63**
regulation of humoral immune response	**136**	**0**	**8.96**	**< 0.01**	**-**	**0.000259**	**0.0225**	**0.123**	**0.929**

Table E12B. Gene Co-Expression and Overrepresentation Test Results: PC2-SA (FDR-corrected) and PC1-SA comparison

First, genome-wide significant (p ≤ 5*10-8) SNPs were mapped to genes using FUMA GWAS [1], resulting in 46 and 34 genes for PC1-SA and PC2-SA, respectively. Gene lists were filtered by the BrainSpan database of 52,376 genes, and one gene present in both lists was excluded, resulting in 44 and 31 genes for PC1-SA and PC2-SA, respectively. In order to identify gene co-expression networks, the top 0.1% positively correlated genes in BrainSpan [2] (filtered for prenatal and cortical samples) were retained for each "seed gene" in the PC1-SA and PC2-SA lists, seperately. Subsequently, the genes unique to PC1-SA and PC2-SA, respectively, were retained. Enrichment analyses for biological processes were conducted on each of the PC-SA lists using the PANTHER Overrepresentation Test (Released 20190711) and the GO Ontology database (Released 2019-07-03) [3]. An FDR correction was applied for multiple comparisons. The **FDR-corrected PC2-SA** results are indicated below, with corresponding PC1.SA p-values for these GO terms.

[1] K. Watanabe, E. Taskesen, A. van Bochoven and D. Posthuma. Functional mapping and annotation of genetic associations with FUMA. Nat. Commun. 8:1826. (2017).

[2] BrainSpan Atlas of the Developing Human Brain Miller, J.A. et al. (2014) Transcriptional landscape of the prenatal human brain, Nature 508: 199-206. doi:10.1038/nature13185

[3] PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. Huaiyu Mi, Anushya

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
cellular response to nicotine	**9**	**5**	**0.48**	**10.31**	**+**	**4.70E-04**	**3.24E-02**	**1**	**1**
cellular process	14514	903	781.83	1.15	+	2.72E-15	1.44E-11	1.37E-12	1.22E-09
telencephalon regionalization	**13**	**6**	**0.7**	**8.57**	**+**	**2.69E-04**	**2.09E-02**	**1**	**1**
forebrain development	392	41	21.12	1.94	+	1.49E-04	1.28E-02	0.000836	0.0554
anatomical structure development	5399	391	290.83	1.34	+	1.45E-10	1.92E-07	5.13E-06	0.00086
developmental process	5749	412	309.68	1.33	+	1.09E-10	1.58E-07	4.94E-07	0.000108
brain development	742	71	39.97	1.78	+	1.01E-05	1.50E-03	1.19E-05	0.00176
head development	786	78	42.34	1.84	+	1.18E-06	2.79E-04	2.82E-05	0.00371
central nervous system development	982	86	52.9	1.63	+	3.21E-05	3.65E-03	0.000125	0.0124
nervous system development	2351	191	126.64	1.51	+	3.18E-08	1.49E-05	7.98E-07	0.000161
system development	4413	334	237.72	1.41	+	6.43E-11	1.02E-07	2.22E-05	0.00304
multicellular organism development	5012	367	269.98	1.36	+	2.09E-10	2.38E-07	8.75E-06	0.00134
multicellular organismal process	6944	442	374.06	1.18	+	3.87E-05	4.22E-03	0.157	1
animal organ development	3188	251	171.73	1.46	+	1.45E-09	1.05E-06	0.00235	0.113
regionalization	334	43	17.99	2.39	+	1.27E-06	2.94E-04	0.658	1
pattern specification process	433	50	23.32	2.14	+	2.80E-06	5.57E-04	0.122	1

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
forebrain regionalization	24	9	1.29	6.96	+	2.92E-05	3.39E-03	1	1
3'-UTR-mediated mRNA destabilizatior	**16**	**6**	**0.86**	**6.96**	**+**	**6.47E-04**	**4.26E-02**	**1**	**1**
mRNA destabilization	30	8	1.62	4.95	+	5.64E-04	3.74E-02	0.0218	0.552
positive regulation of catabolic process	433	42	23.32	1.8	+	6.56E-04	4.29E-02	0.122	1
regulation of catabolic process	990	83	53.33	1.56	+	1.56E-04	1.31E-02	0.00281	0.131
regulation of metabolic process	6707	447	361.29	1.24	+	1.70E-07	5.77E-05	4.87E-16	1.55E-12
regulation of biological process	11660	741	628.09	1.18	+	3.34E-11	5.91E-08	2.33E-14	3.71E-11
biological regulation	12352	778	665.37	1.17	+	1.70E-11	3.86E-08	5.63E-17	8.95E-13
positive regulation of metabolic process	3614	253	194.68	1.3	+	1.64E-05	2.12E-03	0.000105	0.0107
positive regulation of biological process	6166	418	332.15	1.26	+	1.04E-07	3.85E-05	7.83E-06	0.00122
positive regulation of cellular metabolic pr	3314	232	178.52	1.3	+	4.40E-05	4.54E-03	0.00992	0.335
positive regulation of cellular process	5409	371	291.37	1.27	+	3.08E-07	8.75E-05	2.53E-07	5.67E-05
regulation of cellular process	10941	688	589.36	1.17	+	1.02E-08	5.79E-06	1.12E-14	1.98E-11
regulation of cellular metabolic process	6245	414	336.4	1.23	+	1.59E-06	3.55E-04	7.00E-13	7.42E-10
regulation of RNA metabolic process	3826	266	206.1	1.29	+	1.47E-05	1.95E-03	3.09E-13	4.10E-10
regulation of macromolecule metabolic pr	6180	408	332.9	1.23	+	2.88E-06	5.65E-04	6.34E-16	1.68E-12
regulation of nucleobase-containing compc	4080	283	219.78	1.29	+	8.23E-06	1.28E-03	1.41E-13	2.04E-10
regulation of primary metabolic process	6051	397	325.95	1.22	+	8.99E-06	1.36E-03	4.98E-12	3.44E-09
regulation of nitrogen compound metaboli	5868	384	316.09	1.21	+	1.89E-05	2.39E-03	3.92E-12	2.83E-09
regulation of gene expression	4495	309	242.13	1.28	+	5.05E-06	8.74E-04	1.47E-15	3.34E-12
positive regulation of RNA metabolic proce	1719	140	92.6	1.51	+	2.67E-06	5.60E-04	5.87E-05	0.00682
positive regulation of nucleobase-containir	1881	150	101.32	1.48	+	3.86E-06	7.06E-04	9.33E-05	0.00989
positive regulation of nitrogen compound r	3173	225	170.92	1.32	+	2.67E-05	3.15E-03	0.00431	0.18
positive regulation of macromolecule meta	3343	238	180.08	1.32	+	1.07E-05	1.56E-03	3.90E-05	0.00496
negative regulation of gene expression	1716	126	92.44	1.36	+	7.29E-04	4.66E-02	1.06E-07	2.44E-05
negative regulation of macromolecule met	2644	188	142.43	1.32	+	1.44E-04	1.26E-02	2.65E-07	5.85E-05
negative regulation of metabolic process	2890	207	155.68	1.33	+	3.42E-05	3.81E-03	1.28E-07	2.90E-05
negative regulation of biological process	5276	367	284.2	1.29	+	7.91E-08	3.07E-05	3.65E-09	1.09E-06
negative regulation of cellular metabolic pr	2546	190	137.15	1.39	+	8.06E-06	1.27E-03	1.66E-05	0.00242
negative regulation of cellular process	4701	330	253.23	1.3	+	2.65E-07	7.80E-05	3.70E-08	9.64E-06
negative regulation of nitrogen compound	2346	176	126.37	1.39	+	1.46E-05	1.95E-03	0.00054	0.04

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
regulation of cellular macromolecule biosy	3952	271	212.88	1.27	+	3.14E-05	3.59E-03	3.60E-13	4.09E-10
regulation of cellular biosynthetic process	4216	285	227.1	1.25	+	4.84E-05	4.88E-03	3.35E-12	2.54E-09
regulation of biosynthetic process	4296	295	231.41	1.27	+	1.02E-05	1.51E-03	1.56E-11	9.93E-09
regulation of macromolecule biosynthetic p	4082	278	219.89	1.26	+	3.91E-05	4.23E-03	1.44E-12	1.20E-09
negative regulation of cellular macromolec	1390	107	74.88	1.43	+	4.07E-04	2.90E-02	2.06E-05	0.00285
negative regulation of cellular biosynthetic	1525	116	82.15	1.41	+	3.64E-04	2.65E-02	2.81E-05	0.00373
negative regulation of biosynthetic process	1550	118	83.49	1.41	+	3.23E-04	2.38E-02	4.04E-05	0.0051
negative regulation of macromolecule bios	1471	112	79.24	1.41	+	4.56E-04	3.17E-02	2.63E-05	0.00351
CENP-A containing nucleosome assemb	**31**	**9**	**1.67**	**5.39**	**+**	**1.50E-04**	**1.28E-02**	**0.466**	**1**
cellular component organization	5658	420	304.78	1.38	+	4.30E-13	1.37E-09	4.78E-11	2.37E-08
cellular component organization or biogen	5850	434	315.12	1.38	+	1.25E-13	4.98E-10	3.19E-13	3.90E-10
chromosome organization	1056	103	56.88	1.81	+	3.30E-08	1.50E-05	1.91E-15	3.79E-12
organelle organization	3410	265	183.69	1.44	+	1.42E-09	1.07E-06	1.25E-12	1.17E-09
protein-containing complex subunit organi	1851	149	99.71	1.49	+	2.54E-06	5.45E-04	0.0458	0.814
DNA replication-independent nucleosome	40	12	2.15	5.57	+	9.26E-06	1.39E-03	0.748	1
DNA replication-independent nucleosome	41	12	2.21	5.43	+	1.14E-05	1.64E-03	0.359	1
chromatin assembly or disassembly	154	20	8.3	2.41	+	7.06E-04	4.57E-02	0.0158	0.469
cellular component assembly	2528	207	136.18	1.52	+	3.31E-09	2.10E-06	0.0557	0.884
cellular component biogenesis	2758	225	148.57	1.51	+	7.63E-10	6.39E-07	0.00419	0.178
DNA packaging	177	23	9.53	2.41	+	2.68E-04	2.11E-02	0.0255	0.617
DNA conformation change	294	38	15.84	2.4	+	3.51E-06	6.65E-04	2.90E-05	0.00378
cellular protein-containing complex assemb	838	75	45.14	1.66	+	5.82E-05	5.82E-03	0.0412	0.776
protein-containing complex assembly	1566	127	84.36	1.51	+	1.17E-05	1.64E-03	0.141	1
CENP-A containing chromatin organization	31	9	1.67	5.39	+	1.50E-04	1.27E-02	0.466	1
centromere complex assembly	38	9	2.05	4.4	+	5.42E-04	3.62E-02	0.0196	0.534
chromatin remodeling at centromere	34	9	1.83	4.91	+	2.69E-04	2.09E-02	0.294	1
regulation of polysaccharide biosynthe	**38**	**9**	**2.05**	**4.4**	**+**	**5.42E-04**	**3.64E-02**	**0.0522**	**0.849**
cell differentiation in spinal cord	**55**	**12**	**2.96**	**4.05**	**+**	**1.33E-04**	**1.17E-02**	**1**	**1**
spinal cord development	108	16	5.82	2.75	+	5.86E-04	3.87E-02	0.442	1
cell differentiation	3703	256	199.47	1.28	+	3.34E-05	3.77E-03	0.00414	0.178
cellular developmental process	3798	267	204.59	1.31	+	5.63E-06	9.43E-04	0.00287	0.131

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
regulation of sister chromatid segregat	**84**	**17**	**4.52**	**3.76**	**+**	**1.35E-05**	**1.83E-03**	**0.0173**	**0.491**
regulation of chromosome segregation	107	20	5.76	3.47	+	6.88E-06	1.12E-03	0.012	0.387
regulation of cell cycle process	761	81	40.99	1.98	+	3.98E-08	1.76E-05	9.15E-08	2.17E-05
regulation of cell cycle	1190	118	64.1	1.84	+	1.23E-09	9.76E-07	6.72E-08	1.64E-05
regulation of chromosome organization	351	38	18.91	2.01	+	1.58E-04	1.32E-02	4.72E-06	0.000815
regulation of organelle organization	1284	104	69.17	1.5	+	8.83E-05	8.26E-03	1.00E-07	2.35E-05
regulation of cellular component organizat	2455	189	132.24	1.43	+	1.46E-06	3.31E-04	2.61E-09	8.00E-07
mitotic sister chromatid segregation	**105**	**20**	**5.66**	**3.54**	**+**	**5.37E-06**	**9.09E-04**	**0.00177**	**0.0912**
sister chromatid segregation	138	24	7.43	3.23	+	2.62E-06	5.56E-04	0.00434	0.181
nuclear chromosome segregation	215	30	11.58	2.59	+	1.12E-05	1.61E-03	0.000151	0.0145
chromosome segregation	270	40	14.54	2.75	+	7.22E-08	2.94E-05	0.000104	0.0107
cell cycle process	979	94	52.74	1.78	+	3.51E-07	9.62E-05	1.59E-09	5.48E-07
cell cycle	1323	134	71.27	1.88	+	2.66E-11	5.29E-08	5.39E-10	2.09E-07
mitotic cell cycle process	600	75	32.32	2.32	+	2.26E-10	2.40E-07	2.10E-09	6.97E-07
mitotic cell cycle	687	80	37.01	2.16	+	1.55E-09	1.08E-06	2.40E-11	1.37E-08
mitotic nuclear division	141	25	7.6	3.29	+	1.20E-06	2.81E-04	0.000488	0.0368
nuclear division	279	39	15.03	2.59	+	4.49E-07	1.19E-04	0.00081	0.0546
organelle fission	306	41	16.48	2.49	+	7.63E-07	1.93E-04	0.00201	0.1
positive regulation of mitotic cell cycle	**78**	**14**	**4.2**	**3.33**	**+**	**2.31E-04**	**1.87E-02**	**0.648**	**1**
regulation of mitotic cell cycle phase transi	415	45	22.35	2.01	+	3.63E-05	4.01E-03	3.78E-05	0.00485
regulation of cell cycle phase transition	450	49	24.24	2.02	+	1.22E-05	1.69E-03	7.56E-05	0.0084
regulation of mitotic cell cycle	630	72	33.94	2.12	+	2.33E-08	1.16E-05	2.26E-06	0.000403
positive regulation of cell cycle phase trans	95	15	5.12	2.93	+	4.77E-04	3.27E-02	0.681	1
positive regulation of cell cycle process	290	35	15.62	2.24	+	3.36E-05	3.76E-03	0.00237	0.113
positive regulation of cell cycle	385	46	20.74	2.22	+	2.36E-06	5.20E-04	0.00573	0.221
positive regulation of mitotic cell cycle	151	23	8.13	2.83	+	2.82E-05	3.30E-03	0.142	1
mitotic spindle organization	**74**	**13**	**3.99**	**3.26**	**+**	**4.59E-04**	**3.17E-02**	**0.637**	**1**
microtubule cytoskeleton organization invo	103	16	5.55	2.88	+	3.68E-04	2.66E-02	0.236	1
microtubule cytoskeleton organization	463	50	24.94	2	+	1.52E-05	1.98E-03	0.259	1
cytoskeleton organization	1084	92	58.39	1.58	+	4.17E-05	4.45E-03	0.0211	0.539
microtubule-based process	653	65	35.18	1.85	+	8.88E-06	1.36E-03	0.0215	0.548

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
G2/M transition of mitotic cell cycle	**134**	**23**	**7.22**	**3.19**	**+**	**5.11E-06**	**8.73E-04**	**0.0035**	**0.155**
cell cycle G2/M phase transition	136	23	7.33	3.14	+	6.34E-06	1.05E-03	0.00207	0.102
cell cycle phase transition	280	40	15.08	2.65	+	2.16E-07	7.01E-05	5.05E-05	0.00608
mitotic cell cycle phase transition	272	39	14.65	2.66	+	2.96E-07	8.57E-05	0.000113	0.0115
centrosome cycle	**82**	**14**	**4.42**	**3.17**	**+**	**3.64E-04**	**2.65E-02**	**0.00087**	**0.057**
mitotic prometaphase	**170**	**28**	**9.16**	**3.06**	**+**	**1.04E-06**	**2.54E-04**	**0.00131**	**0.0754**
mitotic cell cycle phase	267	39	14.38	2.71	+	2.41E-07	7.51E-05	0.00147	0.0812
cell cycle phase	267	39	14.38	2.71	+	2.41E-07	7.36E-05	0.00147	0.0809
biological phase	267	39	14.38	2.71	+	2.41E-07	7.66E-05	0.00147	0.0815
regulation of mitotic nuclear division	**171**	**25**	**9.21**	**2.71**	**+**	**2.39E-05**	**2.86E-03**	**0.00245**	**0.116**
regulation of nuclear division	196	26	10.56	2.46	+	8.07E-05	7.68E-03	0.00437	0.181
cell division	**495**	**72**	**26.66**	**2.7**	**+**	**1.02E-12**	**2.69E-09**	**0.00508**	**0.2**
central nervous system neuron differe	**183**	**26**	**9.86**	**2.64**	**+**	**4.22E-05**	**4.44E-03**	**0.552**	**1**
neuron differentiation	1011	95	54.46	1.74	+	7.56E-07	1.94E-04	0.0287	0.655
generation of neurons	1541	141	83.01	1.7	+	4.52E-09	2.76E-06	0.000724	0.0514
neurogenesis	1640	148	88.34	1.68	+	3.26E-09	2.16E-06	0.000845	0.0558
response to UV	**144**	**20**	**7.76**	**2.58**	**+**	**4.55E-04**	**3.17E-02**	**0.0962**	**1**
regulation of cell division	**167**	**23**	**9**	**2.56**	**+**	**1.57E-04**	**1.31E-02**	**0.0629**	**0.933**
response to estradiol	**139**	**19**	**7.49**	**2.54**	**+**	**7.09E-04**	**4.55E-02**	**0.605**	**1**
mitotic anaphase	**156**	**21**	**8.4**	**2.5**	**+**	**3.78E-04**	**2.71E-02**	**0.152**	**1**
mitotic M phase	170	25	9.16	2.73	+	2.19E-05	2.66E-03	0.124	1
M phase	170	25	9.16	2.73	+	2.19E-05	2.68E-03	0.124	1
anaphase	156	21	8.4	2.5	+	3.78E-04	2.72E-02	0.152	1
regulation of microtubule cytoskeletor	**196**	**25**	**10.56**	**2.37**	**+**	**2.85E-04**	**2.19E-02**	**0.00105**	**0.0647**
regulation of microtubule-based process	230	30	12.39	2.42	+	4.45E-05	4.56E-03	0.00247	0.116
anterior/posterior pattern specificatio	**218**	**27**	**11.74**	**2.3**	**+**	**1.84E-04**	**1.50E-02**	**0.34**	**1**
regulation of cell cycle G2/M phase tra	**211**	**26**	**11.37**	**2.29**	**+**	**2.63E-04**	**2.08E-02**	**0.00023**	**0.0208**
negative regulation of neuron differen	**228**	**28**	**12.28**	**2.28**	**+**	**1.50E-04**	**1.28E-02**	**0.144**	**1**
negative regulation of neurogenesis	294	34	15.84	2.15	+	1.10E-04	9.82E-03	0.41	1
negative regulation of cell development	338	38	18.21	2.09	+	7.23E-05	7.10E-03	0.582	1
regulation of cell development	946	90	50.96	1.77	+	7.41E-07	1.93E-04	0.0035	0.156

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
regulation of cell differentiation	1814	157	97.72	1.61	+	1.53E-08	8.09E-06	0.00598	0.227
regulation of developmental process	2571	216	138.49	1.56	+	1.71E-10	2.10E-07	0.00076	0.0532
negative regulation of cell differentiation	712	65	38.35	1.69	+	8.93E-05	8.31E-03	0.54	1
negative regulation of nervous system deve	313	34	16.86	2.02	+	2.97E-04	2.24E-02	0.361	1
regulation of multicellular organismal proc	3130	238	168.6	1.41	+	7.85E-08	3.12E-05	0.00112	0.066
regulation of nervous system development	932	83	50.2	1.65	+	2.11E-05	2.62E-03	0.000669	0.0479
regulation of multicellular organismal deve	2037	174	109.73	1.59	+	5.35E-09	3.15E-06	0.0033	0.149
regulation of neurogenesis	824	76	44.39	1.71	+	1.83E-05	2.35E-03	0.00184	0.0932
regulation of neuron differentiation	658	62	35.44	1.75	+	6.52E-05	6.45E-03	0.0178	0.501
rhythmic process	**274**	**33**	**14.76**	**2.24**	**+**	**6.21E-05**	**6.17E-03**	**0.333**	**1**
DNA replication	**211**	**25**	**11.37**	**2.2**	**+**	**5.24E-04**	**3.55E-02**	**8.78E-08**	**2.12E-05**
macromolecule metabolic process	6181	433	332.95	1.3	+	6.18E-10	5.46E-07	7.97E-11	3.62E-08
organic substance metabolic process	7853	513	423.02	1.21	+	1.17E-07	4.14E-05	6.12E-08	1.54E-05
metabolic process	8396	544	452.27	1.2	+	8.34E-08	3.16E-05	2.26E-09	7.19E-07
cellular metabolic process	7663	520	412.79	1.26	+	2.29E-10	2.28E-07	5.12E-11	2.40E-08
cellular macromolecule metabolic process	5088	357	274.08	1.3	+	5.51E-08	2.31E-05	1.00E-12	9.96E-10
heart development	**526**	**57**	**28.33**	**2.01**	**+**	**3.40E-06**	**6.52E-04**	**0.0049**	**0.2**
circulatory system development	867	86	46.7	1.84	+	2.54E-07	7.64E-05	0.00235	0.113
muscle structure development	**481**	**51**	**25.91**	**1.97**	**+**	**1.52E-05**	**2.00E-03**	**0.197**	**1**
embryonic organ development	**431**	**45**	**23.22**	**1.94**	**+**	**7.97E-05**	**7.64E-03**	**0.0261**	**0.627**
embryo development	979	92	52.74	1.74	+	1.07E-06	2.57E-04	0.000886	0.0575
developmental growth	**394**	**41**	**21.22**	**1.93**	**+**	**1.59E-04**	**1.31E-02**	**0.0676**	**0.939**
growth	399	41	21.49	1.91	+	2.55E-04	2.03E-02	0.0702	0.964
reproductive structure development	**424**	**44**	**22.84**	**1.93**	**+**	**1.09E-04**	**9.86E-03**	**0.0967**	**1**
reproductive system development	427	45	23	1.96	+	7.33E-05	7.16E-03	0.118	1
developmental process involved in reprodu	668	59	35.98	1.64	+	4.26E-04	3.00E-02	0.386	1
reproductive process	1426	115	76.81	1.5	+	4.21E-05	4.46E-03	0.00216	0.105
reproduction	1429	115	76.98	1.49	+	4.30E-05	4.50E-03	0.00153	0.0824
regulation of binding	**379**	**39**	**20.42**	**1.91**	**+**	**2.88E-04**	**2.21E-02**	**0.35**	**1**
negative regulation of cell cycle proces	**331**	**34**	**17.83**	**1.91**	**+**	**7.08E-04**	**4.56E-02**	**4.83E-05**	**0.00596**
regulation of Wnt signaling pathway	**362**	**37**	**19.5**	**1.9**	**+**	**4.95E-04**	**3.38E-02**	**0.243**	**1**

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
negative regulation of organelle organi	**382**	**39**	**20.58**	**1.9**	**+**	**3.17E-04**	**2.38E-02**	**0.0503**	**0.831**
negative regulation of cellular component (	705	66	37.98	1.74	+	4.00E-05	4.30E-03	0.00104	0.0644
chordate embryonic development	**636**	**64**	**34.26**	**1.87**	**+**	**6.91E-06**	**1.11E-03**	**0.00104**	**0.0647**
embryo development ending in birth or egg	654	66	35.23	1.87	+	4.17E-06	7.53E-04	0.00156	0.0836
skeletal system development	**494**	**49**	**26.61**	**1.84**	**+**	**1.07E-04**	**9.76E-03**	**0.784**	**1**
DNA repair	**512**	**50**	**27.58**	**1.81**	**+**	**1.37E-04**	**1.20E-02**	**9.21E-09**	**2.62E-06**
DNA metabolic process	745	65	40.13	1.62	+	3.22E-04	2.39E-02	2.04E-10	8.33E-08
nucleobase-containing compound metabol	2788	194	150.18	1.29	+	3.40E-04	2.49E-02	1.69E-12	1.34E-09
organic cyclic compound metabolic process	3243	222	174.69	1.27	+	2.53E-04	2.02E-02	2.11E-09	6.86E-07
cellular nitrogen compound metabolic proc	3425	229	184.5	1.24	+	7.37E-04	4.67E-02	5.09E-11	2.45E-08
nitrogen compound metabolic process	7006	472	377.4	1.25	+	1.26E-08	6.89E-06	4.15E-09	1.22E-06
heterocycle metabolic process	2968	204	159.88	1.28	+	4.10E-04	2.90E-02	1.82E-11	1.07E-08
cellular aromatic compound metabolic pro	3008	208	162.03	1.28	+	2.68E-04	2.10E-02	1.81E-11	1.11E-08
primary metabolic process	7495	493	403.74	1.22	+	1.06E-07	3.83E-05	6.24E-08	1.55E-05
cellular response to DNA damage stimulus	778	71	41.91	1.69	+	4.49E-05	4.58E-03	7.53E-10	2.79E-07
cellular response to stress	1704	136	91.79	1.48	+	1.16E-05	1.64E-03	2.22E-06	0.000407
embryonic morphogenesis	**569**	**55**	**30.65**	**1.79**	**+**	**9.18E-05**	**8.49E-03**	**0.0275**	**0.632**
anatomical structure morphogenesis	2145	187	115.55	1.62	+	2.86E-10	2.68E-07	0.000227	0.0203
cardiovascular system development	**518**	**49**	**27.9**	**1.76**	**+**	**3.21E-04**	**2.39E-02**	**0.0266**	**0.636**
organelle localization	**578**	**54**	**31.14**	**1.73**	**+**	**2.22E-04**	**1.80E-02**	**0.00016**	**0.0155**
cellular localization	2453	194	132.14	1.47	+	1.58E-07	5.47E-05	5.22E-07	0.000112
localization	5737	366	309.04	1.18	+	2.90E-04	2.21E-02	0.000117	0.0118
cell projection morphogenesis	**493**	**46**	**26.56**	**1.73**	**+**	**6.91E-04**	**4.50E-02**	**0.00206**	**0.101**
cell projection organization	1148	102	61.84	1.65	+	2.38E-06	5.20E-04	1.05E-05	0.00157
cell morphogenesis	721	67	38.84	1.73	+	4.72E-05	4.78E-03	0.000296	0.0247
cellular component morphogenesis	826	75	44.49	1.69	+	3.70E-05	4.06E-03	0.000892	0.0577
cell part morphogenesis	514	49	27.69	1.77	+	2.96E-04	2.24E-02	0.00188	0.0948
animal organ morphogenesis	**965**	**89**	**51.98**	**1.71**	**+**	**2.79E-06**	**5.69E-04**	**0.0481**	**0.841**
cell morphogenesis involved in differer	**557**	**51**	**30**	**1.7**	**+**	**5.09E-04**	**3.46E-02**	**0.00213**	**0.104**
cell development	1641	135	88.4	1.53	+	2.80E-06	5.63E-04	0.0307	0.684
sensory organ development	**552**	**50**	**29.73**	**1.68**	**+**	**6.96E-04**	**4.52E-02**	**0.3**	**1**

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
viral process	**700**	**61**	**37.71**	**1.62**	**+**	**5.47E-04**	**3.64E-02**	**0.0213**	**0.544**
symbiotic process	782	69	42.12	1.64	+	1.72E-04	1.41E-02	0.0109	0.362
interspecies interaction between organism	826	72	44.49	1.62	+	1.42E-04	1.24E-02	0.0334	0.718
apoptotic process	**904**	**78**	**48.7**	**1.6**	**+**	**1.07E-04**	**9.81E-03**	**0.196**	**1**
cell death	1070	85	57.64	1.47	+	7.35E-04	4.68E-02	0.659	1
regulation of anatomical structure mor	**1067**	**92**	**57.48**	**1.6**	**+**	**2.63E-05**	**3.12E-03**	**0.0443**	**0.8**
anatomical structure formation involve	**884**	**76**	**47.62**	**1.6**	**+**	**1.64E-04**	**1.35E-02**	**0.00498**	**0.2**
plasma membrane bounded cell projec	**1105**	**95**	**59.52**	**1.6**	**+**	**1.99E-05**	**2.49E-03**	**9.52E-06**	**0.00144**
neuron development	**817**	**70**	**44.01**	**1.59**	**+**	**3.19E-04**	**2.38E-02**	**0.00447**	**0.185**
peptidyl-amino acid modification	**898**	**76**	**48.37**	**1.57**	**+**	**2.47E-04**	**1.98E-02**	**6.25E-05**	**0.0071**
cellular protein modification process	3106	226	167.31	1.35	+	4.69E-06	8.30E-04	0.00505	0.199
protein modification process	3106	226	167.31	1.35	+	4.69E-06	8.20E-04	0.00505	0.199
protein metabolic process	4326	300	233.03	1.29	+	3.72E-06	6.88E-04	0.00931	0.321
organonitrogen compound metabolic proc	5332	347	287.22	1.21	+	1.03E-04	9.47E-03	0.0356	0.713
macromolecule modification	3326	238	179.16	1.33	+	7.04E-06	1.12E-03	0.00355	0.156
cellular protein metabolic process	3730	261	200.93	1.3	+	1.21E-05	1.69E-03	0.00129	0.0742
positive regulation of transcription by	**1214**	**101**	**65.4**	**1.54**	**+**	**4.34E-05**	**4.51E-03**	**0.00097**	**0.0616**
regulation of transcription by RNA polymer	2699	196	145.39	1.35	+	2.98E-05	3.44E-03	6.51E-09	1.88E-06
regulation of transcription, DNA-templated	3516	241	189.4	1.27	+	1.10E-04	9.86E-03	7.98E-11	3.52E-08
regulation of nucleic acid-templated transc	3574	245	192.52	1.27	+	8.77E-05	8.25E-03	3.95E-11	2.09E-08
regulation of RNA biosynthetic process	3579	246	192.79	1.28	+	7.43E-05	7.21E-03	4.09E-11	2.10E-08
positive regulation of transcription, DNA-te	1547	128	83.33	1.54	+	3.61E-06	6.75E-04	7.77E-05	0.00846
positive regulation of gene expression	1998	157	107.63	1.46	+	4.28E-06	7.66E-04	1.07E-06	0.000208
positive regulation of nucleic acid-templat	1634	130	88.02	1.48	+	2.20E-05	2.65E-03	0.000263	0.0225
positive regulation of RNA biosynthetic pro	1635	131	88.07	1.49	+	1.34E-05	1.84E-03	0.000265	0.0224
positive regulation of cellular biosynthetic	1985	149	106.93	1.39	+	8.10E-05	7.67E-03	0.00135	0.0759
positive regulation of biosynthetic process	2018	151	108.7	1.39	+	7.46E-05	7.19E-03	0.00202	0.1
positive regulation of macromolecule biosy	1899	147	102.29	1.44	+	1.88E-05	2.39E-03	0.00177	0.0914
positive regulation of cell differentiatio	**968**	**79**	**52.14**	**1.52**	**+**	**5.29E-04**	**3.56E-02**	**0.0869**	**1**
positive regulation of developmental proce	1361	116	73.31	1.58	+	3.04E-06	5.90E-04	0.116	1
cellular protein localization	**1598**	**130**	**86.08**	**1.51**	**+**	**8.28E-06**	**1.28E-03**	**5.01E-06**	**0.00085**

GO.BIOLOGICAL.PROCESS.COMPLETE	Ref.20996	PC2.SA.BS	expected	Fold Enrichment	direction	PC2.raw.p	PC2.FDR.p	PC1_p	PC1_fdr
protein localization	2153	163	115.98	1.41	+	2.13E-05	2.62E-03	7.53E-07	0.000156
macromolecule localization	2489	179	134.08	1.34	+	1.17E-04	1.04E-02	7.63E-06	0.00123
cellular macromolecule localization	1606	131	86.51	1.51	+	6.65E-06	1.09E-03	6.71E-06	0.0011
positive regulation of cellular compone	**1206**	**96**	**64.96**	**1.48**	**+**	**2.70E-04**	**2.08E-02**	**7.65E-05**	**0.00839**
intracellular transport	**1522**	**118**	**81.99**	**1.44**	**+**	**1.45E-04**	**1.26E-02**	**0.00567**	**0.219**
establishment of localization in cell	1834	144	98.79	1.46	+	1.36E-05	1.83E-03	5.17E-05	0.00619
establishment of protein localization	**1609**	**121**	**86.67**	**1.4**	**+**	**4.07E-04**	**2.89E-02**	**0.00053**	**0.0392**
positive regulation of multicellular org	**1742**	**129**	**93.84**	**1.37**	**+**	**4.33E-04**	**3.03E-02**	**0.176**	**1**
Unclassified	**3181**	**81**	**171.35**	**0.47**	**-**	**1.41E-15**	**1.12E-11**	**5.73E-17**	**3.04E-13**
G protein-coupled receptor signaling p	**1302**	**28**	**70.14**	**0.4**	**-**	**1.72E-08**	**8.82E-06**	**3.00E-04**	**0.0246**
adaptive immune response	**602**	**7**	**32.43**	**0.22**	**-**	**1.86E-07**	**6.16E-05**	**6.42E-07**	**0.00014**
detection of chemical stimulus involve	**430**	**3**	**23.16**	**0.13**	**-**	**4.42E-07**	**1.19E-04**	**8.59E-10**	**3.10E-07**
detection of chemical stimulus involved in	480	3	25.86	0.12	-	4.98E-08	2.14E-05	3.90E-11	2.14E-08
sensory perception of chemical stimulus	532	4	28.66	0.14	-	2.60E-08	1.25E-05	9.55E-10	3.37E-07
detection of chemical stimulus	517	5	27.85	0.18	-	3.14E-07	8.77E-05	1.95E-09	6.61E-07
detection of stimulus involved in sensory p	538	7	28.98	0.24	-	2.69E-06	5.56E-04	1.17E-11	7.72E-09
sensory perception of smell	460	4	24.78	0.16	-	9.83E-07	2.44E-04	1.21E-10	5.07E-08

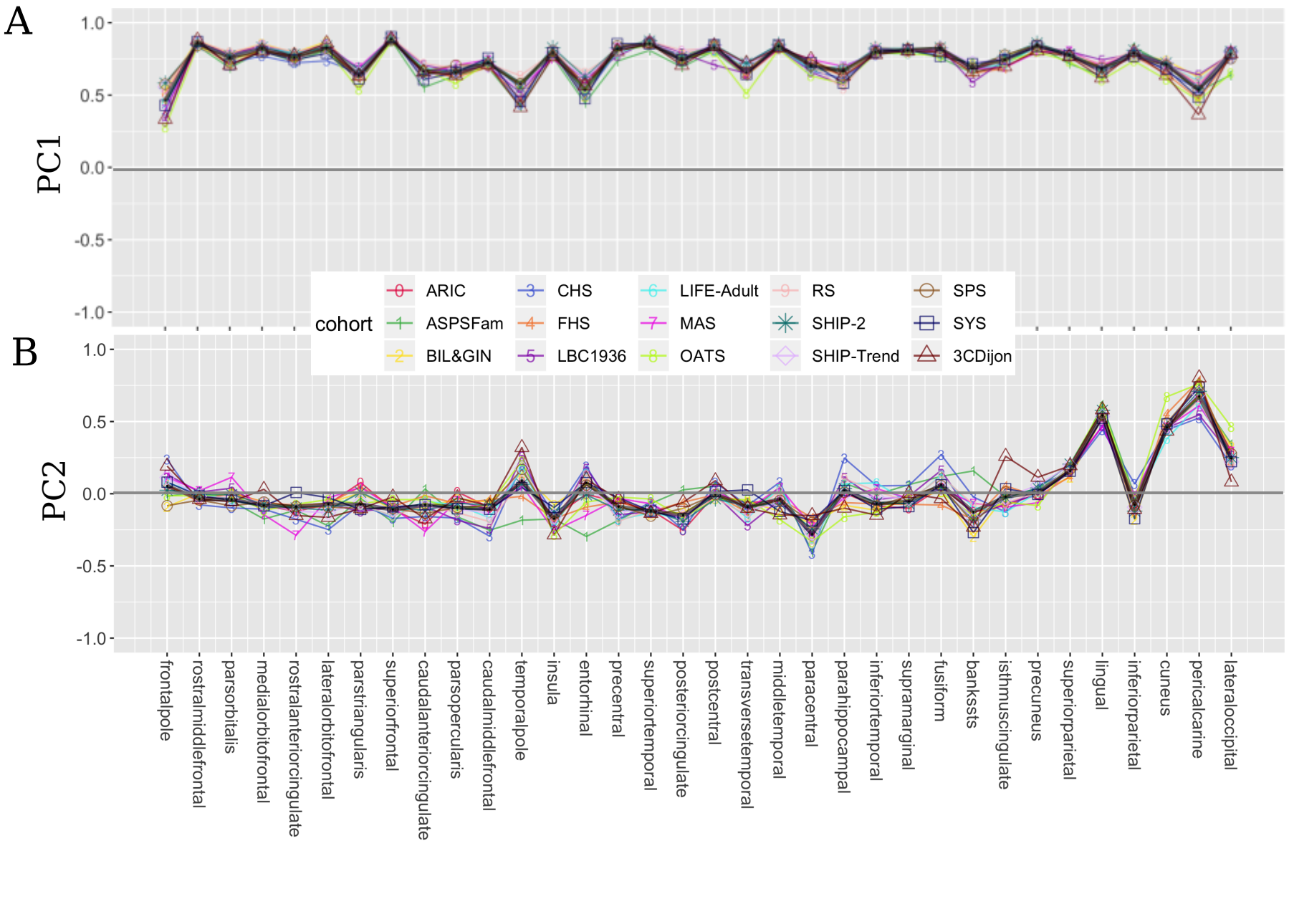
Cortical Plate)

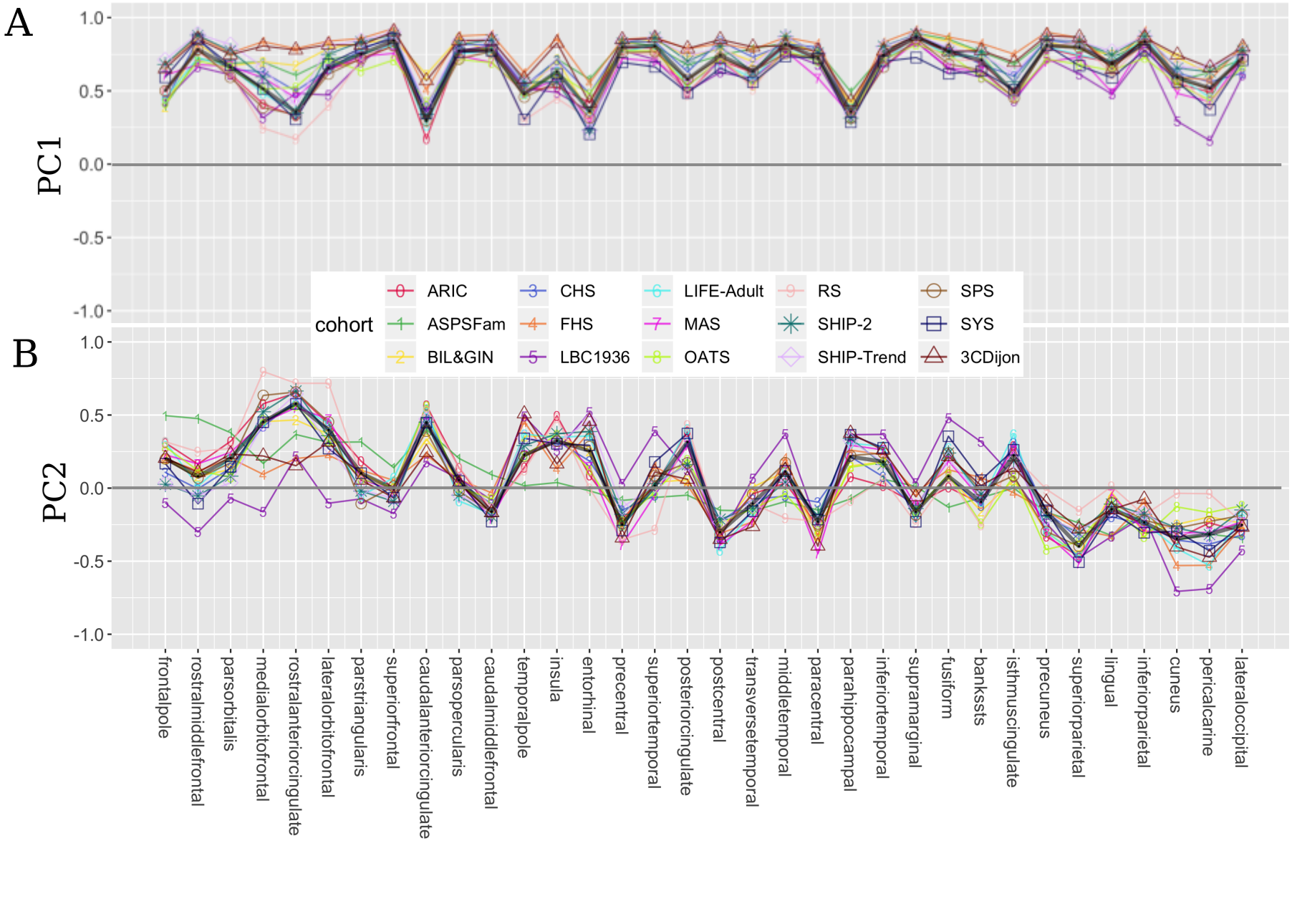
Partitioned heritability (LD score regression (LDSC) v1.0.0 [1]) was conducted to assess the enrichment of PC1-SA and PC2-SA GWAS variants in chromatin regions with differential accessibility during cortical neurogenesis between the germinal zone (GZ) and cortical plate (CP), as reported previously for other phenotypes [2]. Enrichment of heritability represents the ratio between (i) the proportion of heritability explained by a particular annotation and (ii) the proportion of SNPs in the annotation [1,2]. An annotation file was generated for regions in which chromatin was more accessible in GZ, compared to CP (GZ>CP; 19,260) and vice-versa (CP>GZ; 17,803), using the available supplementary data table [2]. Next, LD scores for the chromatin annotation file were computed following the LDSC guidelines (https://github.com/bulik/ldsc/wiki/LD-Score-Estimation-Tutorial), using the available HapMap3 SNPs, a 1 cM window, and the Phase 3 1000 Genomes European genotype files. Finally, partitioned heritability was run combining the chromatin annotation file with the LDSC baseline annotation file. The required LDSC files were obtained from the LDSC GitHub repository (https://data.broadinstitute.org/alkesgroup/LDSCORE/).

[1] Finucane, H.K. et al. Partitioning heritability by functional annotation using genome-wide association summary statistics. Nat Genet 47, 1228 (2015).

[2] de la Torre-Ubieta, L. et al. The dynamic landscape of open chromatin during human cortical neurogenesis. Cell 172, 289-304. e18

GWAS	Category	Prop. SNPs	Prop h2	Prop h2 Standard Error (SE)	Enrichment	Enrichment SE	Enrichment P
PC1-SA	GZ>CP	0.0072	0.1039	0.0367	14.4007	5.0950	**5.27E-03**
PC1-SA	CP>GZ	0.0068	0.0683	0.0333	10.0518	4.8960	5.71E-02
PC2-SA	GZ>CP	0.0072	0.0967	0.0384	13.4088	5.3308	**1.88E-02**
PC2-SA	CP>GZ	0.0068	0.0457	0.0337	6.7247	4.9607	2.39E-01


A
PC1
1.0
0.5
0.0
-0.5
-1.0
cohort
ARIC
ASPSFam
BIL&GIN
CHS
FHS
LBC1936
LIFE-Adult
MAS
OATS
RS
SHIP-2
SHIP-Trend
SPS
SYS
3CDijon
B
PC2
1.0
0.5
0.0
-0.5
-1.0
frontalpole
rostralmiddlefrontal
parsorbitalis
medialorbitofrontal
rostralanteriorcingulate
lateralorbitofrontal
parstriangularis
superiorfrontal
caudalanteriorcingulate
parsopercularis
caudalmiddlefrontal
temporalpole
insula
entorhinal
precentral
superiortemporal
posteriorcingulate
postcentral
transversetemporal
middletemporal
paracentral
parahippocampal
inferiortemporal
supramarginal
fusiform
bankssts
isthmuscingulate
precuneus
superiorparietal
lingual
inferiorparietal
cuneus
pericalcarine
lateraloccipital


A
B
PC1
PC2
1.0
0.5
0.0
-0.5
-1.0
cohort
ARIC
ASPSFam
BIL&GIN
CHS
FHS
LBC1936
LIFE-Adult
MAS
OATS
RS
SHIP-2
SHIP-Trend
SPS
SYS
3CDijon
frontalpole
rostralmiddlefrontal
parsorbitalis
medialorbitofrontal
rostralanteriorcingulate
lateralorbitofrontal
parstriangularis
superiorfrontal
caudalanteriorcingulate
parsopercularis
caudalmiddlefrontal
temporalpole
insula
entorhinal
precentral
superiortemporal
posteriorcingulate
postcentral
transversetemporal
middletemporal
paracentral
parahippocampal
inferiortemporal
supramarginal
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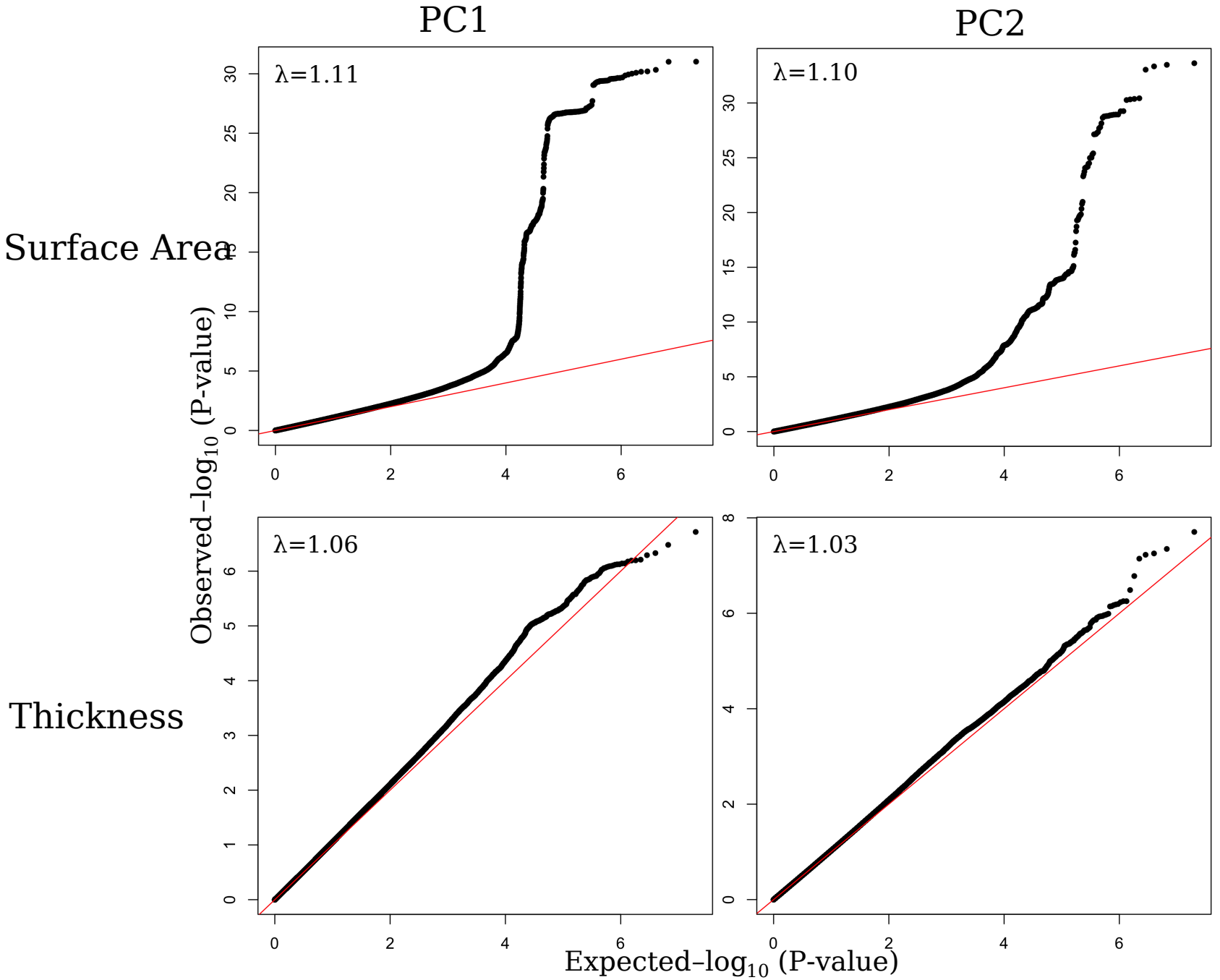
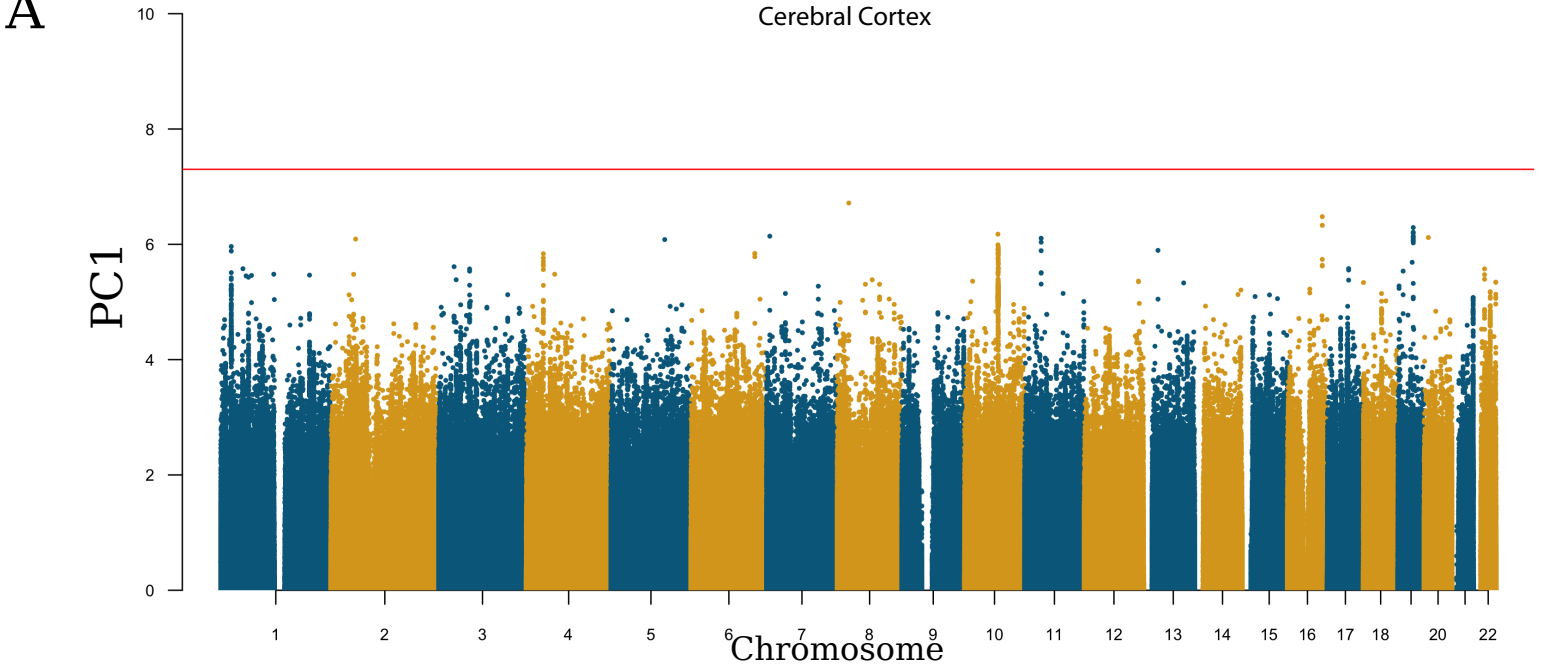
pericalcarine
lateraloccipital


PC1
PC2
Surface Area
Thickness
λ=1.11
λ=1.10
λ=1.06
λ=1.03
Observed–log10 (P-value)
Expected–log10 (P-value)


A
PC1
Chromosome
0
2
4
6
8
10
1
2
3
4
5
6
7
8
9
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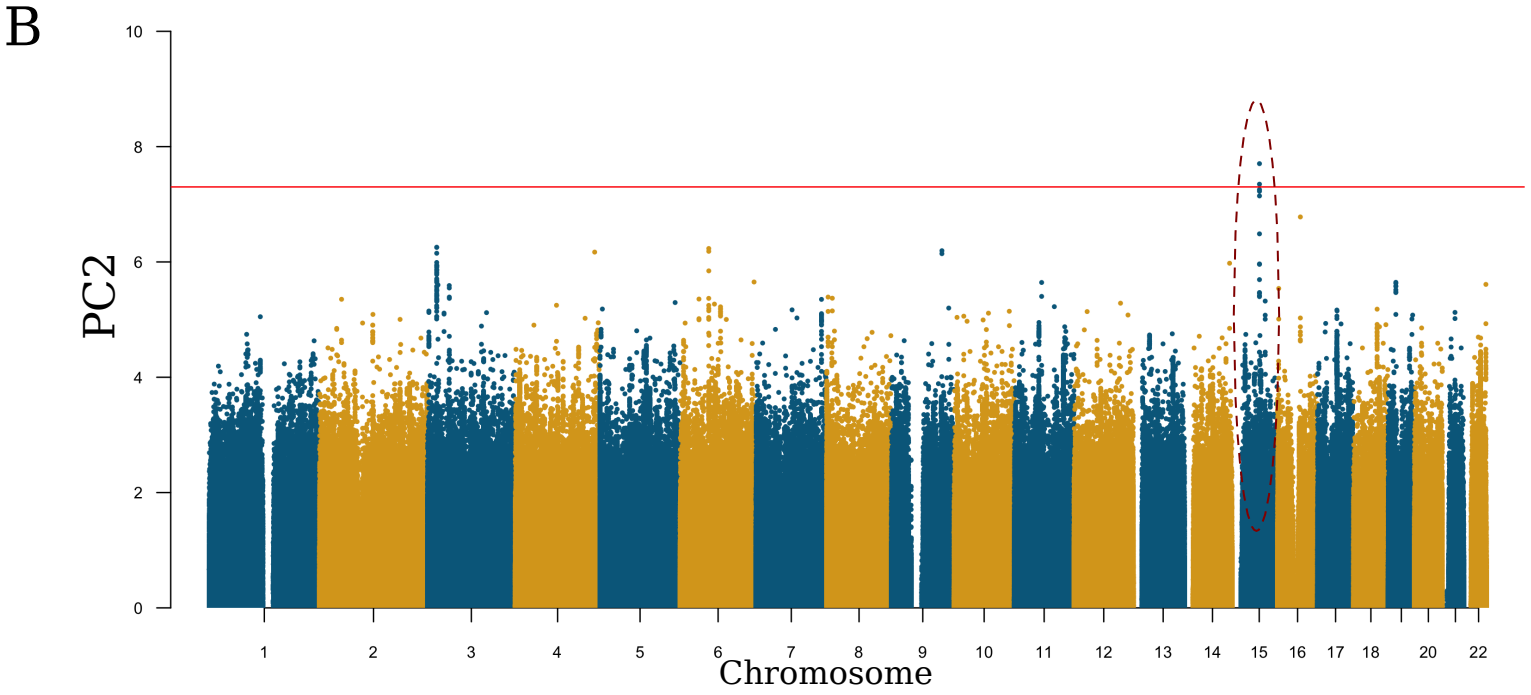
16
17
18
20
22


B
PC2
Chromosome
0
2
4
6
8
10
1
2
3
4
5
6
7
8
9
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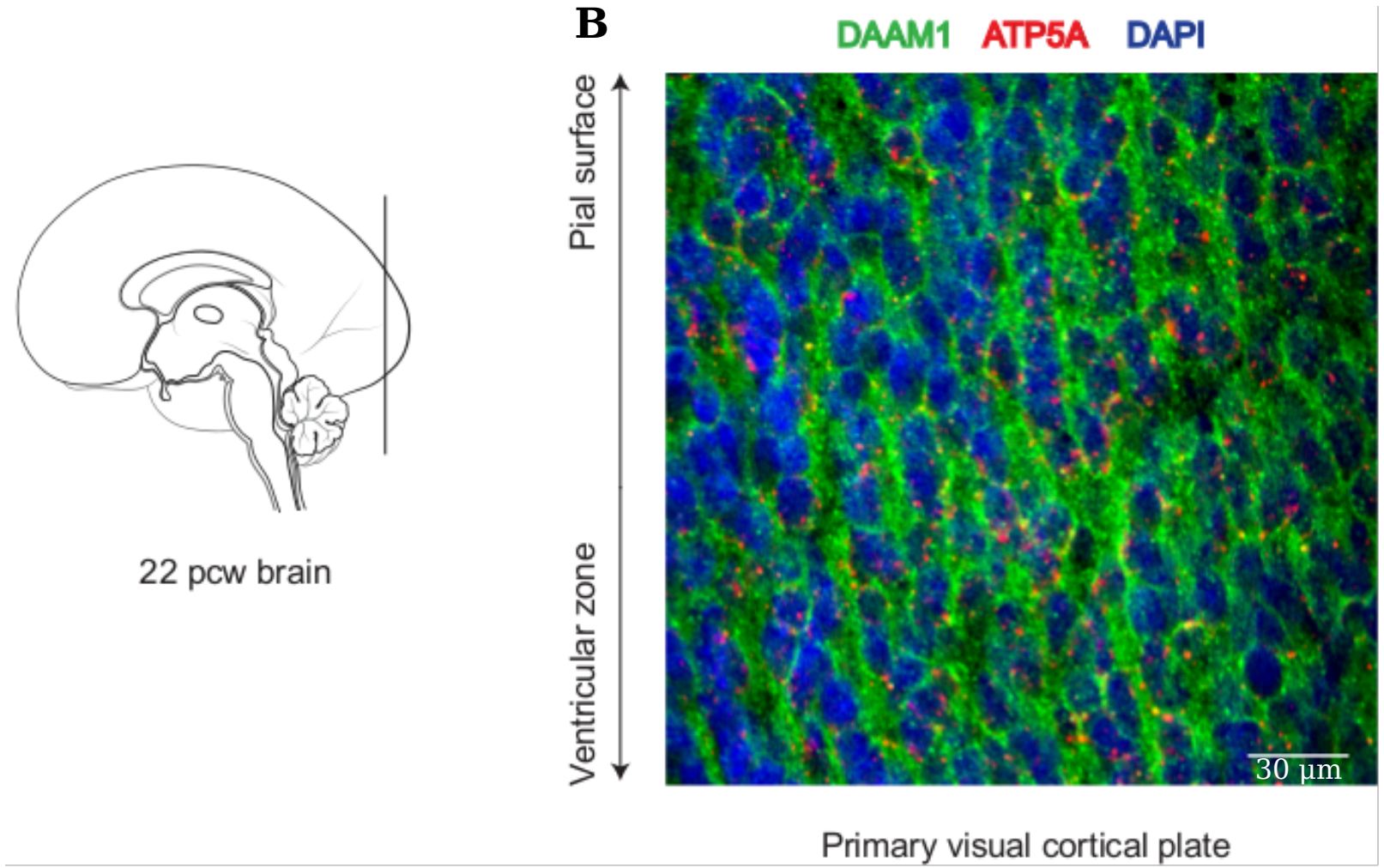
16
17
18
20
22


A
22 pcw brain
B
DAAM1 ATP5A DAPI
Pial surface
Ventricular zone
30 µm
Primary visual cortical plate